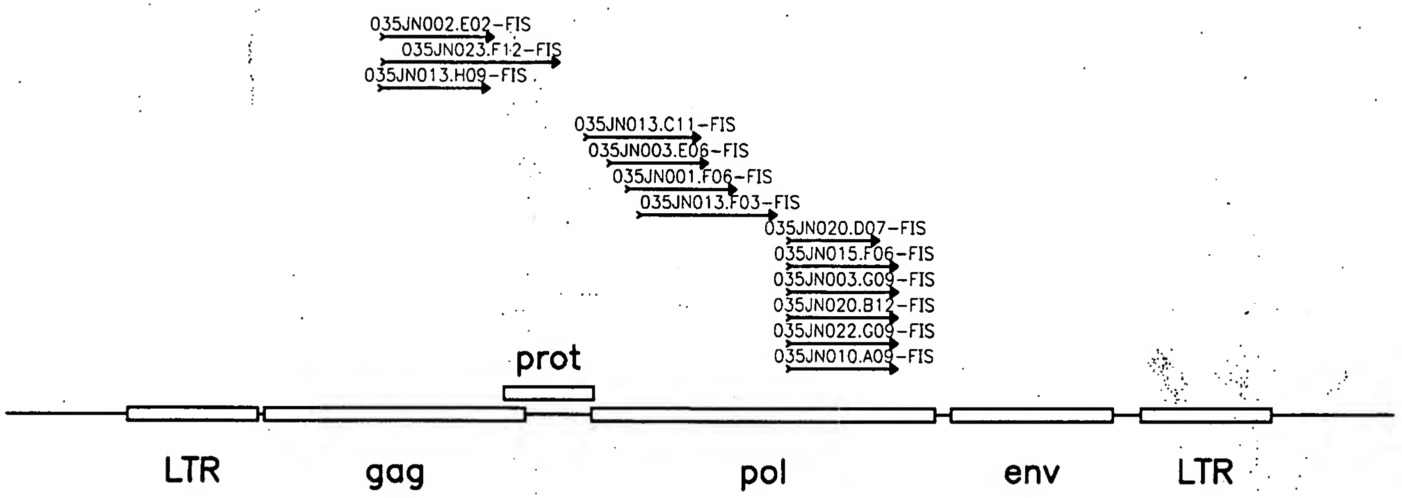

035JN002.E02–FIS
035JN023.F12–FIS
035JN013.H09–FIS
035JN013.C11–FIS
035JN003.E06–FIS
035JN001.F06–FIS
035JN013.F03–FIS
035JN020.D07–FIS
035JN015.F06–FIS
035JN003.G09–FIS
035JN020.B12–FIS
035JN022.G09–FIS
035JN010.A09–FIS
prot
LTR
gag
pol
env
LTR

FIG. 1

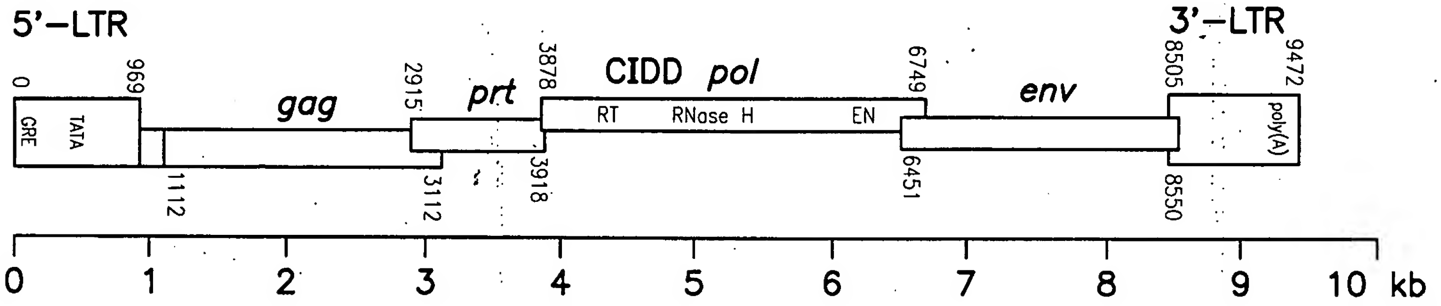
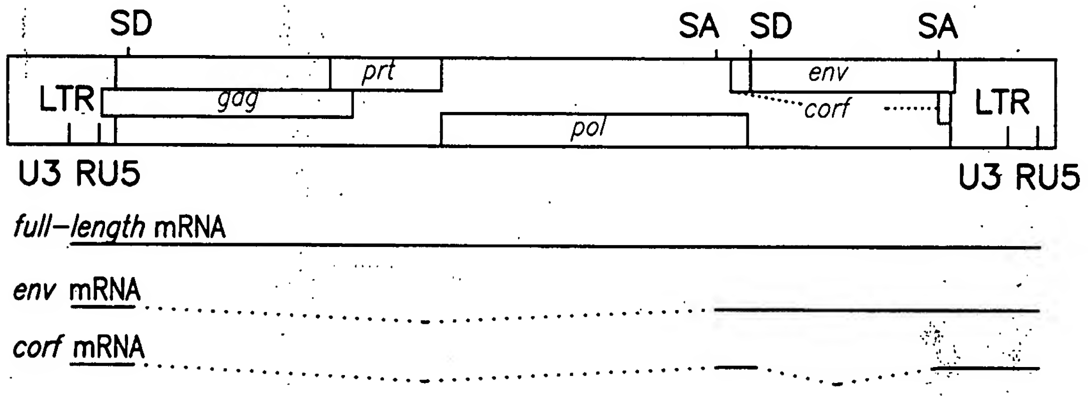
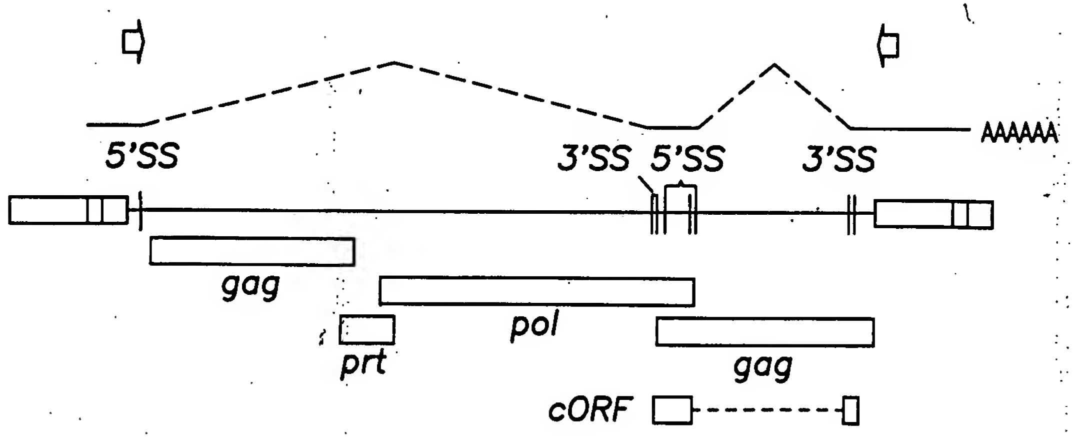

5'–LTR
0
GRE
TATA
969
1112
gag
2915
3112
prt
3878
3918
CIDD pol
RT
RNase H
EN
6749
6451
env
3'–LTR
8505
8550
9472
poly(A)
0
1
2
3
4
5
6
7
8
9
10 kb

FIG. 2



SD
SA
SD
SA
prt
env
LTR
gag
corf
LTR
pol
U3 RU5
U3 RU5
full–length mRNA
env mRNA
corf mRNA

FIG. 3



AAAAAA
5'SS
3'SS
5'SS
3'SS
gag
pol
prt
gag
cORF

FIG. 4

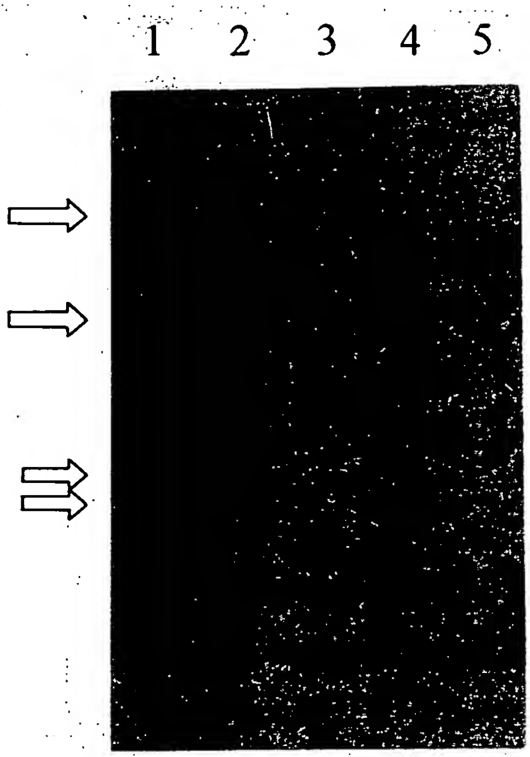


FIG. 5

```
                                       1                                                                              80
        ENV GENOMIC HERV MDA    (1) ---------------------------------------------------------------ACATTTAAAGTTCTACA
     ENV GENOMIC HERV-K TAN.    (1) ---------------------------------------------------------------ACATTTGAAGTTCTACA
        ENV GENOMIC AC025420    (1) ---------------------------------------------------------------ACATTTGAAGTTCTACA
        ENV GENOMIC AP000776    (1) ---------------------------------------------------------------ACATTTGAAGTTCTACA
         ENV GENOMIC HERV-K8    (1) --------------------------------------------------------------------------------
         ENV GENOMIC HERV-KI    (1) ---------------------------------------------------------------ACATTTGAAGTTCTACA
         ENV HERV-K AF023261    (1) GGGGAGAGGTTTTGCTTGTGTTTCACCAGGAGAAAATCAGCTTCCTGTTTGGATACCCACTAGACATTTGAAGTTCTACA
            ENV GEN AL035086    (1) --------------------------------------------------------------------------------
        ENV GENOMIC AL035587    (1) ---------------------------------------------------------------AAATTTAAAGTTCTACA
        ENV GENOMIC AC012068    (1) ---------------------------------------------------------------------------CTACA
        ENV GENOMIC AF277315    (1) ------------------------------------------------------------------TTTAAAGTTCTACA
        ENV GENOMIC AF027650    (1) GGGGAGAGGTTTTGCTTGTGTTTCACCAGGAGAAAATCAGCTTCCTGTTTGGATACCCACTAGACATTTGA--TTCTACA
        ENV GENOMIC AC078899    (1) ---------------------------------------------------------------ACATTTGA--TTCTACA
        ENV GENOMIC HERV-KII    (1) ---------------------------------------------------------------ACATTTGAAGTTCTACA
        ENV GENOMIC AC008813    (1) ----------------------------------------------------ATACCCACTAGACATTTAAAGTTCTACA
        ENV GENOMIC AC012309    (1) ------------------------------------------------------------TAGACATTTGAAGTTCTACA
        ENV GENOMIC AL121932    (1) ---------------------------------------------------------------ACATTTGAAGTTCTACA
        ENV GENOMIC AD000090    (1) ---------------------------------------------------------------ACATTTGAAGTTCTACA
           ENV GEN  AL160008    (1) --------------------------------------------------------------------------------
        ENV GENOMIC HEU32496    (1) ---GCGTAATCATTGAGGACAAGTCGACGAGAGATCCCGAGGACGTCTACAGTCAGCCTTACGACATTTGAAGTTCTACA
        ENV GENOMIC AC011467    (1) ------GGTTTTGCTTGTGTTTCACGAGGAGA-AAATCAGCTTCCTGTTTGGATGCCCACTAGACATTTGAAGTTCTACA
        ENV GENOMIC AF235103    (1) --------TTTTTCTTGTGTTTCACCAGGAGA-AAATCAGCTTCCTGTTTGGATACCCACTAGACATTTGAAGTTCTACA
        ENV GENOMIC AC026786    (1) --------TTTTGCTTGTGTTTAACCAGAAAATAAATCAGCTTCCAGTTTGGATACTTACAACTT---------------
        ENV GENOMIC AC034203    (1) ----------------------CACCAGGAGA-AAATCAGCTTCCTGTTTGGGTACCCACTAGACATTTGAAGTTCTACA
        ENV GENOMIC AC018809    (1) -----------------------------------------------------------------ATTTGAAGTTCTACA
ENV GENOMIC HERV-K102 AF164610  (1) ----------TTGCTTGTGTTTCACCAGGAGA-AAATCAGCTTCCTGTTTGGATACCCACTAGACATTTGAAGTTCTACA
   ENV GENOMIC FRAG. AF260253   (1) --------------------------------------------------------------------------------
                   CONSENSUS    (1)                                                                ACATTTGAAGTTCTACA
```

FIG. 6-1

```
                                    81                                                                             160
          ENV GENOMIC HERV MDA (18) ATGAACTCACTGGAGATGCAAAGAAA----------AGT------GTGGAGATGGAGACACCCCAATCGA----------
       ENV GENOMIC HERV-K TAN. (18) ATGAACCCATCAGAGATGCAAAGAAA----------AGCACCTCCGCGGAGACGGAGACATCGCAATCGAGCACC-----
          ENV GENOMIC AC025420 (18) ATGCACCCATCGGAGATGCAAAGAAA----------AGCACCTCCGCGGAGACGGAGACACCGCAATCGAGCACC-----
          ENV GENOMIC AP000776 (18) ATGAACCCATCAGAGATGCAAAGAAA----------AGCACCTCCGCGGAGACGGAGACACCGCAATCGAGCACC-----
           ENV GENOMIC HERV-K8  (1) -------------------------------------------------------------CGCAATCGAGCACC-----
           ENV GENOMIC HERV-KI (18) ATGAACTCATCAGAGATGCAAAGAAA----------AGCACATCCGTGGAGACGGAGACACCACAATCGAGCACC-----
           ENV HERV-K AF023261 (81) ATGAACCCATCGGAGATGCAAAGAAA----------AGCACCTCCGCGGAGACGGAGACACCGCAATCGAGCACC-----
               ENV GEN AL035086 (1) --------------------------------------------------------------------------------
          ENV GENOMIC AL035587 (18) ATGAACCCCTTGGAGATGCGAAGAAA----------AGCGCCTCTGCGGAGACAAAAAACCCTCAATTGAGCATC-----
          ENV GENOMIC AC012068  (6) ATGAACCCATCAGAGATGCAAATGAA----------GGTGCCTCCATAGAGACAGAAAACCTGCAATCGAGCATC-----
          ENV GENOMIC AF277315 (15) ATGAACCCATCGGAAATGCAAAGAAA----------AGCGCCTCCGCGGAGACAGAAAACCCGCAATCGAGCATC-----
          ENV GENOMIC AF027650 (79) ATGAACCCATCGGAGATGCAAAGGAA----------AGCACCTCCACGGAGACGGAAACACCGCAATTGAACACC-----
          ENV GENOMIC AC078899 (16) ATGAACCCATCGGAGATGCAAAGGAA----------AGCACCTCCACGGAGACGGAAACACCGCAATTGAACACC-----
          ENV GENOMIC HERV-KII (18) ATGAACCCATCGGAGATGCAAAGAAA----------AGGGCCTCCACAGAGATGGTAACCCCAG----------------
          ENV GENOMIC AC008813 (29) ATGAACCCATTAGAGATGCAAACAAACAAAAAAAAAAGCGCCTCCACAGAGACGGAAACACCGCAATCGAGCACC-----
          ENV GENOMIC AC012309 (21) ATGAACCTGTCGGAGATGCAAAGAAA----------AGCACCTCCACGGAGACAGAAACACTGCAATCAAGCACC-----
          ENV GENOMIC AL121932 (18) ATGAACCCATCGGAGATGCAAAGAAA----------AGCGCCTCCACGGAGATGGAAACACAGCAATCGAGCACC-----
          ENV GENOMIC AD000090 (18) ATGAACCCATCAGAGATGCAAAGAAA----------AGCACCTCCACGGAGACGGAGACACCGCAATCGAGCACCGTCAT
              ENV GEN  AL160008 (1) --------------------------------------------------------------------------------
          ENV GENOMIC HEU32496 (78) ATGCACCCATCGGAGATGCAAAGAAA----------AGCACCTCCGCGGAGACGGAGACACCGCAATCGAGCACC-----
          ENV GENOMIC AC011467 (74) ATGAACCCATCGGAGATGAAAAGAAA----------AGCGCCTCCATGGAGATGGAAACACCAC----------------
          ENV GENOMIC AF235103 (72) ATAAACCCATCCCATCAGAAATGCAA----A-TAAAAGTGCCTCCACAGAGACAAAAAACCTGCAGTTGAGCATC-----
          ENV GENOMIC AC026786 (58) --------------------------------------------------------------------------------
          ENV GENOMIC AC034203 (58) ATGAACCCATCAGAGATACAAAGGAA----------GGCGCCTCTGCAGAGACAAAAAACCCACAATCGAACATC-----
          ENV GENOMIC AC018809 (16) ATGAATCCATCAGAGATGCAAAGAAA----------AGCGCCTCCACGGACATGGAAACACCAG----------------
ENV GENOMIC HERV-K102 AF164610 (70) ATGAACCCATTGGAGATGCAAAGAAA----------AGGGCCTCCACGGAGATGGTAACACCAG----------------
    ENV GENOMIC FRAG. AF260253  (1) --------------------------------------------------------------------------------
                     CONSENSUS (81) ATGAACCCATC GAGATGCAAAGAAA          AGC CCTCC CGGAGACGGAAACACCGCAATCGAGCA C
```

FIG. 6-2

```
                                    161                                                                            240
        ENV GENOMIC HERV MDA   (72) -------------CTCGCCAGGTAAACAAAATGGTGATATCAGAAGAACAGAAAAAGTTGCCTTCCATCAAGGAAGCAGA
     ENV GENOMIC HERV-K TAN.   (83) --------GTTGACTCACAAGATGAACAAAATGGTGACGTCAGAAGAACAGATGAAGTTGCCATCCACCAAGAAGGCAGA
        ENV GENOMIC AC025420   (83) --------GTTGACTCACAAGATGAACAAAATGGTGACATCAGAA---CAGATGAAGTTGCCATCCACCAAGAAGGCAGA
        ENV GENOMIC AP000776   (83) --------GTTGACTCACAAGATGAACAAAATGGTGACGTCAGAAGAACAGATGAAGTTGCCATCCACCAAGAAGGCAGA
         ENV GENOMIC HERV-K8   (15) --------GTTGACTCACAAGATGAACAAAATGGTGACGTCAGAAGAACAGATGAAGTTGCCATCCACCAAGAAAGCAGA
         ENV GENOMIC HERV-KI   (83) --------GTTGACTCACAAGATGAACAAAATGGTGACGTCAGAAGAAGAGATGAAGTTGCCATCCACCAAGAAGGCAGA
         ENV HERV-K AF023261  (146) --------GTTGACTCACAAGATGAACAAAATGGTGACGTCAGAAGAACAGATGAAGTTGCCATCCACCAAGAAAGCAGA
            ENV GEN AL035086    (1) --------------------------------------------------------------------------------
        ENV GENOMIC AL035587   (83) --------ATCGACTCGCCAGGTAAATAAAATGGTGATATCAGAAGAACAGATGAAGTTGCCATCCACCAAGGAAGCGGA
        ENV GENOMIC AC012068   (71) --------ATCACCTCGCCAGGTGAAGAAAATGGTGATATCAAAAGAACAGATGAAGTTGCCATCCACCAAGAAAGCGGA
        ENV GENOMIC AF277315   (80) --------ATCGACTCGCCAGGTGAACAAAATGGTGGTATCAGAAGAACAGATGAAGTTGACATCCACCAAGGAAGTGGA
        ENV GENOMIC AF027650  (144) --------ATTGACTCATAAGATGAAGAAAAAGGTCATGTCAGAAGAACAGATGAAGTTGCCTTCCACCAAGAAGACAGA
        ENV GENOMIC AC078899   (81) --------ATTGACTCATAAGATGAAGAAAAAGGTCATGTCAGAAGAACAGATGAAGTTGCCATCCACCAAGAAGACAGA
        ENV GENOMIC HERV-KII   (72) --------------------------------------------------------------------------------
        ENV GENOMIC AC008813  (104) --------ATTGACTCACAAGATAAACAAAATGGTGATGTCAAAAAAACAGATGAAGTTGCCATCCACCACGAAGGCGGA
        ENV GENOMIC AC012309   (86) --------ATCAACTCACAAGAT----AAAATGGTGATGTCAGAAGAATAGATGAAGTTGCCATTCACCAAGAAGGCAGA
        ENV GENOMIC AL121932   (83) --------ATCGACTCACAAGATGAACAGAATGGTGATGTCAGAAGAATAGATGAAGTTGCCATCCACCAAGAAGACAAA
        ENV GENOMIC AD000090   (88) CGAGAACCATCGACTCAGAAGATGAACAGAATGGTGATGTCAGAAGAACAGATGAAGTTGCCATCCACCAAGAAGGCAGA
            ENV GEN  AL160008   (1) -----------------------------------------------ACAGATAAAGTTGTCATCCACCAAGAAAGCGGA
        ENV GENOMIC HEU32496  (143) --------GTTGACTCACAGGATGAACAAAATGGTGACATCAGA---ACAGATGAAGTTGCCATCCACCAAGATGGCAGA
        ENV GENOMIC AC011467  (128) --------------------------------------------------------------------------------
        ENV GENOMIC AF235103  (142) --------ATCGACCCACCAGGTGAACAAAATGGTGATATCAGAAGAACAGATGAAGTTGCCATCCACCAAGAAAGCGGA
        ENV GENOMIC AC026786   (58) -----------------------------------------------ACAAAAGAAGTTTCCATCTACCAAGAAAGCGGA
        ENV GENOMIC AC034203  (123) --------ATCGACTCGCAGGATGAATAAAATGGTAATATCAGAAAAACAGATGAAATTGCCATCCACCAAAAAGGTGGA
        ENV GENOMIC AC018809   (70) --------------------------------------------------------------------------------
ENV GENOMIC HERV-K102 AF164610  (124) --------------------------------------------------------------------------------
  ENV GENOMIC FRAG. AF260253    (1) --------------------------------------------------------------------------------
                   CONSENSUS  (161)          T GACTCACAAGATGAA AAAATGGTGA  TCAGAAGAACAGATGAAGTTGCCATCCACCAAGAA GC GA
```

FIG. 6-3

```
                                         241                                                                           320
ENV GENOMIC HERV MDA               (139) GTTGCCAATATAGGCACAATTAAAGAAGCTGACACAGTTAGCTAAAAAAAAAAGCCTAGAGAATACAAAGGTGACACCAA
ENV GENOMIC HERV-K TAN.            (155) GCCGCCAACTTGGGCACAACTAAAGAAGCTGACGCAGTTAGCTACAAAATA---TCTAGAGAACACAAAGGTGACACAAA
ENV GENOMIC AC025420               (152) GCCGCCGACTTGGGCACAACTAAAGAAGCTGACGCAGTTAGCTACAAAATA---TCTAGAGAACACAAAGGTGACACAAA
ENV GENOMIC AP000776               (155) GCCGCCAACTTGGGCACAACTAAAGAAGCTGACGCAGTTAGCTACAAAATA---TCTAGAGAACACAAAGGTGACACAAA
ENV GENOMIC HERV-K8                 (87) GCCGCCGACTTGGGCACAACTAAAGA-GCTGACGCAGTTAGCTACAAAATA---TCTAGAGAACACAAAGGTGACACAAA
ENV GENOMIC HERV-KI                (155) GCCACCGACTTGGGCACAACTAAAGAAGCTGACACAGTTAGCTACAAAATA---TCTAGAGAACACAAAGGTGACACAAA
ENV HERV-K AF023261                (218) GCCGCCGACTTGGGCACAACTAAAGAAGCTGACGCAGTTAGCTACAAAATA---TCTAGAGAACACAAAGGTGACACAAA
ENV GEN AL035086                     (1) ---------------------------------------------------------------CACAAAGGTGACACAAA
ENV GENOMIC AL035587               (155) GCCACCGACTTGGGCCCAATTAAAGAAGCTGACACAGTTAGCTAAAAAAAG---CCTAAAGAACACAAGGGTAATGTGAA
ENV GENOMIC AC012068               (143) GCCGCCGACCTGGGCCCAGCTAAAGAAGCTGACACAGTTAGCTGAAAAAAG---CCTGAAAAACATGAGGGTAACATAAA
ENV GENOMIC AF277315               (152) GCCGCCGACCTGGGCCCAACTAAAGAAGTTGACACAGTTAGCTGAAAAAAG---CCTGAAGAAAACAAGGGTAACACAAA
ENV GENOMIC AF027650               (216) GCCGCCGACTTGGGCACAATTAAAGAAGGTGACACCGTTAGCTAAAAAAAA--GCCTGGAGAACACAAAGGTGACACAAA
ENV GENOMIC AC078899               (153) GCCGCCGACTTGGGCACAATTAAAGAAGGTGACACCGTTAGCTAAAAAAAA--GCCTGGAGAACACAAAGGTGACACAAA
ENV GENOMIC HERV-KII                (72) --------------------------------------------------------------------------------
ENV GENOMIC AC008813               (176) GATGCCAACTTGGGCACAATTTAA-AAGCTGACACAGTTAGCTTAAAAAAG---CCTAGAGAACACAAAGGTGACACAAA
ENV GENOMIC AC012309               (154) GCCGCCGACTTGGGCACAATTAAAGAAGCTGACACAGTTAGCTAAAAAAGG---CCTTGAGAACACAAAGGTGACACAAA
ENV GENOMIC AL121932               (155) GCTGCTGACTTGGGCACAATTAAAGAAGCTGACGCAGTTAGCTACAAAATG---TCTAGAGAACACAAAGGAGACACAAA
ENV GENOMIC AD000090               (168) GCTGCTGACTTGGGCACAATTAAAGAAGCTGACACAGTTAGCTACAAAATA---TCTAGAGAACACAAAGGTGACACAAA
ENV GEN  AL160008                   (34) GCCGCCGACTTGGGCACAATTAAAGAAGCTGACACAGTTAGCTGAAAAAAG---CCTAAAGAACACAAGGGTAATCCAAA
ENV GENOMIC HEU32496               (212) GCCGCCGACTTGGGCACAACTAAAGAAGCTGACGCAGTTAGCTACAAAATA---TCTAGAGAACACAAAGGTGACACAAA
ENV GENOMIC AC011467               (128) --------------------------------------------------------------------------------
ENV GENOMIC AF235103               (214) GCCGCCAACCTGGGCCCAGCTAAAGAAGCTGACACAGTTAGCTGAAAAAAG---TCTGAAAAACACAAGGGTAACACAAA
ENV GENOMIC AC026786                (91) GCCGTCGACATGGGCCCAGCTAAAGAAGCTGACACAGTTAGCTGAAAAAAA--GCCTGGAAAACACAAGAGTAACACAAA
ENV GENOMIC AC034203               (195) GCTGCCGACCTGGGCCCAGCTAAAGAAGCTGACACAGTTAGCTAAAAAAAG---CCTGGAAAACACAAGGGTAACACAAA
ENV GENOMIC AC018809                (70) --------------------------------------------------------------------------------
ENV GENOMIC HERV-K102 AF164610     (124) --------------------------------------------------------------------------------
ENV GENOMIC FRAG. AF260253           (1) --------------------------------------------------------------------------------
CONSENSUS                          (241) GCCGCCGACTTGGGCACAA TAAAGAAGCTGACACAGTTAGCTA AAAA      CT GAGAACACAAAGGTGACACAAA
```

FIG. 6-4

```
                                       321                                                                            400
           ENV GENOMIC HERV MDA  (219) CTCCAGAGAATATGCTGCTTGCAGCTCTGATGATTGTATCAACGGTGGTAAGTCTTCCCAAGTCTGCAGGAGCAGCTGCA
      ENV GENOMIC HERV-K TAN.    (232) CCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
        ENV GENOMIC AC025420 .   (229) CCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
           ENV GENOMIC AP000776  (232) CCCCAGAGAGTATGCTGCTTGCGGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
            ENV GENOMIC HERV-K8  (163) CCCCAGAGAGTATGCTGCTTGCAGCT-TGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
            ENV GENOMIC HERV-KI  (232) CCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
            ENV HERV-K AF023261  (295) CCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
                ENV GEN AL035086 (18)  CTCCAGAGAATATGCTGCTTGCAGCTTTGATGATTGTATCAACGGTGATAAGTCTTCCCATGTCTGCAGGAGCAGCTGCA
           ENV GENOMIC AL035587  (232) CTCCAGAGAATATACTGCTTACAGCTTTGATTATTATATCAACGGTAGTAAGTCTCCCCATGTCTGCAGGAGCAGCTGCA
           ENV GENOMIC AC012068  (220) CTCCAGAGAATATGCTGCTTGCAGCTTTAATGATTGTATCAATGGTGCTAAGTCTCCCTATATCTGCAGGAGCCGCTACA
           ENV GENOMIC AF277315  (229) CTCCAGAGAATATGCTGCTTGCAGTTTTGATGATTGTATCAATGGTGGTAAGTGTCCCCATGTCTGCAGGAGCAGCTGCA
           ENV GENOMIC AF027650  (294) CTCCAAAGGGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCCATTCCTGCAGGAGCAGCTGTG
           ENV GENOMIC AC078899  (231) CTCCAAAGGGTATGCTGCTTGCAGCTTTGATGATTGTATCAATGGTGGTAAGTCTCCCCATTCCTGCAGGAGCAGCTGTG
           ENV GENOMIC HERV-KII  (72)  --------------------------------------------------------------------------------
           ENV GENOMIC AC008813  (252) CTCCAGAGAACACGCTGCTTGCAGCTTTGATGATTGTATCAACGGTGGTAAGTCTCCCCACGCCTGCAGGAGCAGCTGCA
           ENV GENOMIC AC012309  (231) CTCCAGAGAGTATGCTGCTTGCAGCTTTGATGATTGTATCAATGGTGGTAAGTCTCCCCATGCCTGTAGGAGCAGCTGCA
           ENV GENOMIC AL121932  (232) CTCCAGAGAGTATGCTGCTTGCAGCTTTGATGATTGTATCAACGGTGGT--GTCTCCCCATGCCTGCAGGAGTAGCTGCA
           ENV GENOMIC AD000090  (245) CTCCAGAGAGTATGCTGCTTGCAGCTTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
               ENV GEN  AL160008 (111) CTCCAGAGAATATGCAGCTTGCAGCCTTGATGATTGTGTCAACGGTGGTAAGTCTCCCCAGGCCTGCAGGAGCAACTGCA
           ENV GENOMIC HEU32496  (289) CCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
           ENV GENOMIC AC011467  (128) --------------------------------------------------------------------------------
           ENV GENOMIC AF235103  (291) CTCCAGAGAATATGCTGCTTGCAGCTTTAATGATTGTATCAATGGTGGTAAGTCTCCCTATGTCTGCAGGAGCCGCTACA
           ENV GENOMIC AC026786  (169) CTCCAGAGAATATGCTGCTTGCAGCTTTAATGATTGTATCAACGGTGGTAAGTCTCCCTATGTCTGCAGGAGCCGCTACA
           ENV GENOMIC AC034203  (272) CTCCAGAGAATATGCTGCTTGCAGCTTTAATGATTGTATCAACAGTGGTAAGTCTCCCTACATCTGTGGAGCCGCTAGA
           ENV GENOMIC AC018809  (70)  --------------------------------------------------------------------------------
ENV GENOMIC HERV-K102 AF164610  (124) --------------------------------------------------------------------------------
     ENV GENOMIC FRAG. AF260253  (1)   --------------------------------------------------------------------------------
                       CONSENSUS (321) CTCCAGAGA TATGCTGCTTGCAGCTTTGATGATTGTATCAATGGTGGTAAGTCTCCC ATGCCTGCAGGAGCAGCTGCA
```

FIG. 6-5

```
                                          401                                                                            480
         ENV GENOMIC HERV MDA      (299)  GCTAATTATACTTACTGGGCCTATGTGCCTTTCCCACCCTTAATTCGGGCAGTTACATAGATGGATAATCCTATTGAAGT
      ENV GENOMIC HERV-K TAN.      (312)  GCTAACTATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCTACAGAAGT
         ENV GENOMIC AC025420      (309)  GCTAACTATACCAACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCTATAGAAGT
         ENV GENOMIC AP000776      (312)  GCTAACTATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCTATAGAAGT
          ENV GENOMIC HERV-K8      (242)  GCTAACTATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGG-------------------------------
          ENV GENOMIC HERV-KI      (312)  GCTAACTATACCTACTGGGCCTAAGTGCCTTTCCCGCCCTTAATTTGGGCAGTCACATGGATGGATAATCCTATAGAAGT
          ENV HERV-K AF023261      (375)  GCTAACTATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCTATAGAAGT
             ENV GEN AL035086       (98)  GCTAATTATGCTTACTGGGCCTATGTGCCTTTCCTGCCCTTAATTCGGGCAGTTACATGGGTGGATAATTCTATTGAAGT
         ENV GENOMIC AL035587      (312)  ACTAATTATACTTACTGTGCCTATGTGCCTTTCCCACCCTTAATTTGGGCAGTCACATGGATGGATAATCCTGTTGAAGT
         ENV GENOMIC AC012068      (300)  GCTAACTATACTTACTGGGCCTATGTGCCTTTCCCACCCTTAATTCGGGCACTCACTTGGAGAGATAATCCTATTGAAGT
         ENV GENOMIC AF277315      (309)  GCTAATTATACTTACTGGACCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATAGATAATCCTATTAAAGT
         ENV GENOMIC AF027650      (374)  GCTAATTATACCTACTGGGCCTGTGTGCTTTTCCCGCCCTTAATTCAGGCAGTCACGTGGATGGATAATCCTATTGAAGT
         ENV GENOMIC AC078899      (311)  GCTAATTATACCTACTGGGCCTGTGTGCTTTTCCCGCCCTTAATTCAGGCAGTCACCTGGATGGATAATCCTATTGAAGT
         ENV GENOMIC HERV-KII       (72)  ----------------------------------------------------TCACATGGATGGATAATCCTATAGAAGT
         ENV GENOMIC AC008813      (332)  GCTAATTATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCTCATGGATGGATAATCCTATTGAAGT
         ENV GENOMIC AC012309      (311)  GCTAATTATACCTACTGGGCCTGTGTGCCTTTCCTGCCCTTAATTCGGGCAGTCGCATGGATGGATAATCCTATTGAAGT
         ENV GENOMIC AL121932      (310)  GCTAATTATACCTACTGGGCCTATGTGCCTTTCCTGCCCTTAATTCAG-GAGTCACATGGATGGATAATCCTATTGAATT
         ENV GENOMIC AD000090      (325)  GCTAATTATAATTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCAGGCAGTCACATGGATGGATAATCCTATGGAAGT
             ENV GEN  AL160008     (191)  GCTAATTATGCCTATTGGGCATATGTCCCATTCCTGCCTTTAATTAGGCCTGTCACATGGTTGGAAACCCCGGTTGAGGT
         ENV GENOMIC HEU32496      (369)  GCTAACTATACCAACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCT--------
         ENV GENOMIC AC011467      (128)  ----------------------------------------------------TCACATGGATGGATAATCCTATTGAAGT
         ENV GENOMIC AF235103      (371)  GCTAACTATACTTACTGGGCCTATGTGCCTTTCCGACCCTTAATTCGGGCAGTCACTTGGATAGATAATCCTATTGAAGT
         ENV GENOMIC AC026786      (249)  ACTAACTATACTTACTGGGCCTATGTGCCTTTCCCACCCTTAATTCAGACAATTACTTGGATAGATAATCCTATTGAAGT
         ENV GENOMIC AC034203      (352)  GCTAACTATACTTACTGGGCCTATGTGCCTTTCCCACCCTTAATTCGGGCAGTCACTTGGATAGATAATCCTATTGAAAT
         ENV GENOMIC AC018809       (70)  ----------------------------------------------------TCACATGGATGGATAATCCTATTGAAGT
ENV GENOMIC HERV-K102 AF164610     (124)  ----------------------------------------------------TCACATGGATGGATAATCCTATAGAAAT
   ENV GENOMIC FRAG. AF260253        (1)  --------------------------------------------------------------------------------
                    CONSENSUS      (401)  GCTAA TATAC TACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCTATTGAAGT
```

FIG. 6-6

```
                                        481                                                                              560
         ENV GENOMIC HERV MDA  (379) AGATGTTAATAATAGTGCATGGG-TGCCTGGCCCCACAGATGACTGTTGCCCTGCCCAACCTGA---AGAAGGAATGATG
      ENV GENOMIC HERV-K TAN.  (392) ATATGTTAATGATAGTGTATGGG-TACCTGGCCCCATAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATG
         ENV GENOMIC AC025420  (389) ATATGTTAATGATAGTGTATGGG-TACATGGCCCCATAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATG
         ENV GENOMIC AP000776  (392) ATATGTTAATGATAGTGTATGGG-TACCTGGCCCCATAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATG
          ENV GENOMIC HERV-K8  (291) --------------------------------------------------------------------------------
          ENV GENOMIC HERV-KI  (392) ATATGTTAATGATAGTGTATGGG-TACCTGGCCCCACAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAAGGATGATG
           ENV HERV-K AF023261 (455) ATATGTTAATGATAGTGTATGGG-TACCTGGCCCCACAGATGATCACTGCCCTGCCAAACCTGAGGAAGAAGGGATGATG
             ENV GEN AL035086  (178) ATATGTTAATAATAGTGCATGGG-TACCTGGCCCCACGGATGATCGTTGCCCTGCCCAACCCAAGGAAGAAGGAATGATG
         ENV GENOMIC AL035587  (392) ATATGTTAATAATAGGGCATGGG-TACCAGGCCCCACAGACGATTGTTGCCCTGCCCAACCTAAAGAAGAAGGAATGATG
         ENV GENOMIC AC012068  (380) ACATGTTAACAATAGTACATGGG-TACCAGACCCCACAGATGACCGTGGCCCTGCCCAACCTGAAGAAGAAGGAATGATG
         ENV GENOMIC AF277315  (389) ATGTGTTAATAATAGTGCATGAG-TACCAGGCCCCACAGATGATTGTTGCCCTGCCCAACCTGAAAAAGAAGGAATGATG
         ENV GENOMIC AF027650  (454) ATATGTTAATAATGGTGTATGGG-TACATGGCCCTACAGATGATCGTTGCCCTGCCAAACCCAAGGAAGAAGGAATGATG
         ENV GENOMIC AC078899  (391) ATATGTTAATAATGGTGTATGGG-TACATGGCCCTACAGATGATCGTTGCCCTGCCAAACCCAAGGAAGAAGGAATGATG
         ENV GENOMIC HERV-KII  (100) ATATGTTAATGATAGTGTATGGG-TACCTGGCCCCACAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATG
         ENV GENOMIC AC008813  (412) ATACGTTAATAATAGTGTATGGG-TACCTGGCCCCACAGATGATCGTTGCCCTGCCAAACCTGAGGAAGAAGGAATGATG
         ENV GENOMIC AC012309  (391) ATATGTTAATAACAGTGTATGGG-TACCTGGCCCCACAGATGATCACTGCCCTGCCAAACCTGAGGAAGAAGGAATGACG
         ENV GENOMIC AL121932  (389) ATATGTTAATAATAGCGTGTGGC-TACCTGGCCCCACAGATGATTATTGCCCTGCCAAACCTGAGGAAGAAGGAATGATG
         ENV GENOMIC AD000090  (405) ATATGTTAATGATAGTGTATGGG-TACCTGGTCCAACAGATGATCGTTGCCCTGCCAAACCTGAGGAAGAAGGGATGATG
              ENV GEN AL160008 (271) TTACGTTCATAGTAGTGTTTGGA-TGCCTGAGCCTACAGATTCTCGTGGGCCCTGTCACCCAGAGGAGGAAGGAATGTTA
         ENV GENOMIC HEU32496  (441) --------------------------------------------------------------------------------
         ENV GENOMIC AC011467  (156) ATATGTTAATGATAGTGTATGGG-TACATGGCCCCACAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATG
         ENV GENOMIC AF235103  (451) ATATGTTAATAATAGTGCATGGG-TACCAGGCCCCACAGATGACCGTGGCCCTGCCCAACCTGAAGAAGAAGGAATGATG
         ENV GENOMIC AC026786  (329) ATACGTTAATAACAGTGCATGGG-TACCAGGCCCCATGGATGACCGTGGCCCTGCCCAACCTGA---AGAAGGAATGATG
         ENV GENOMIC AC034203  (432) ATATGTTAATAACAGTGTATGGG-TACCAGGCCCCACAGATAACCGTGGCCCTGCCCAACCTGAAGAAGAAGGAATGATG
         ENV GENOMIC AC018809   (98) ATATGTTAATGATAGTGTATGGGGTACCTGGCCCCACAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATTATG
ENV GENOMIC HERV-K102 AF164610 (152) ATATGTTAATGATAGTGTATGGG-TACCTGGACCCATAGATGATCGCTGCCCTGCCAAACCTGAGGAAGAAGGGATGATG
    ENV GENOMIC FRAG. AF260253   (1) --------------------------------------------------------------------------------
                     CONSENSUS (481) ATATGTTAATAATAGTGTATGGG TACCTGGCCCCACAGATGATCGTTGCCCTGCCAAACCTGAGGAAGAAGGAATGATG
```

FIG. 6-7

```
                                      561                                                                         640
        ENV GENOMIC HERV MDA   (455)  ACGAATATTTCCATTGGGTATCCTTATCCTCCTGTTTGCCTAGGGAAGGCACCAGGATGCTTAAT-GCCTACAACCCAAA
   ENV GENOMIC HERV-K TAN.   (471)  ATAAATATTTCCATTGGGTATCATTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAAT-GCCTGCAGTCCAAA
        ENV GENOMIC AC025420   (468)  ATAAATATCTCCATTGGGTATCATTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAAT-GCCTGCAGTCCAAA
        ENV GENOMIC AP000776   (471)  ATAAATATTTCCATTGGGTATCGTTATCCTCCTATTTGCTTAGGGACAGCACCAGGATGTTTAAT-GCCTGCAGTCCAAA
         ENV GENOMIC HERV-K8   (291)  --------------------------------------------------------------------------------
         ENV GENOMIC HERV-KI   (471)  ATAAATATTTCCATTGGGTATCGTTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAAT-GCCTGCAGTCCAAA
         ENV HERV-K AF023261   (534)  ATAAATATTTCCATTGGGTATCGTTATCCTCCTATTTGCTTAGGGAGAGCACCAGGATGTTTAAT-GCCTGCAGTCCAAA
            ENV GEN AL035086   (257)  ATGATTATTTCCACTGGGTATTGTTATCCTCCTATTTGCCTGGGGAGGGCACCAGGATGCTTAAT-GCCTACAACCCAAA
        ENV GENOMIC AL035587   (471)  ATAAATGTTTCCACTGGGTATCATTATCCTCCTATTTGCCTAGGGAAGGCACCAGGATGTTTAAT-GCCTACAACCCAAA
        ENV GENOMIC AC012068   (459)  ATAAACATTTCCATTGGGTATCATTATCCTCCTATTTGTCTGGGAAAAGCACCAGGATGCTTAAT-GCCTACAAACCAAA
        ENV GENOMIC AF277315   (468)  ATAAATATTTCCATTGGGTATCATTATCCTCCTATTTGCCTAGGGAAGGCACCAGGATATTTAAT-TCCTACAACCCAAA
        ENV GENOMIC AF027650   (533)  ATAAATATCTCCACTGGATATCGCTATCCTCCTATTTGCCTAGGGAGAGCACTAGGATGTTTAAT-GCCTGCAATCCAAA
        ENV GENOMIC AC078899   (470)  ATAAATATCTCCACTGGATATCGTTATCCTCCTATTTGCCTAGGGAGAGCACTAGGATGTTTAAT-GCCTGCAATCCAAA
        ENV GENOMIC HERV-KII   (179)  ATAAATATTTCCATTGTGTATCGTTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAAT-GCCTGCAGTCCAAA
        ENV GENOMIC AC008813   (491)  ATAAATATTTCCACTGGGTATCATTATCCTCCTATTTGCCTCGGGAGAGCACCAGGATGTTTAAT-GCCTGCAGTCAAAA
        ENV GENOMIC AC012309   (470)  ATAAATATTTCTACTGGGTATCGTTATCCTCCTATTTGTCTAGGGAGAACACCAGGATGTTTAAT-GCCTACAATCCAAA
        ENV GENOMIC AL121932   (468)  ATAAATATTTCCACTGGGTATTGTTATCCTCCTATTTGCCTAGGGAGAACACCAGGATGTTTAAT-GCCTGCAATCCAAA
        ENV GENOMIC AD000090   (484)  ATAAATATTTTCATTGGGTATCATTATCCTCCTATTTGCCTGGGGAGAGCACCAGGATGTTTAAT-GCCTGCAGTCCAAA
           ENV GEN  AL160008   (350)  ATAAATGTGTCCGTGGGTTATCAATTCCCCCCTGTTTGCATAGGGCTGGCTATCTGTTGCCTAAAAGGCTACCGAC-AAC
        ENV GENOMIC HEU32496   (441)  --------------------------------------------------------------------------------
        ENV GENOMIC AC011467   (235)  ACAAATATTTCCACTGGGTATCATTATCCTCCTATTTGCCTAGGGAGAGCACTAGGATGCTTAAT-GCCTGCAGTCCAAA
        ENV GENOMIC AF235103   (530)  ATAAACATTTCCATTGGGTATCATTATCCTCCTATTTGCCTGGGAAAAGCACCGGGATGCTTAAT-GCCTACAAACCAAA
        ENV GENOMIC AC026786   (405)  ATAAACATTTCCATTGGGTATCATTATCCTCCTATTTGCCTGGAAAAAGCACCAGGATGCTTAAT-GCCTACAATCCAAA
        ENV GENOMIC AC034203   (511)  ATAAACATTTCCATTGGGTATCATTATCCTCCTATTTGCTTGGGAAAAGCACCAGGATGCTTAAT-GCCTACTATCCAAA
        ENV GENOMIC AC018809   (178)  ATAAATATTTCCACTGGGTATCGTTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGCTTAAT-GCCTGCAGTCCAAA
ENV GENOMIC HERV-K102 AF164610   (231)  ATAAATATTTCCATTGGGTATCGTTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAAT-GCCTGCAGTCCAAA
   ENV GENOMIC FRAG. AF260253     (1)  --------------------------------------------------------------------------------
                   CONSENSUS   (561)  ATAAATATTTCCATTGGGTATC TTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAAT GCCTGCA TCCAAA
```

FIG. 6-8

```
                                     641                                                                            720
      ENV GENOMIC HERV MDA   (534) ATTGGTTGGTAGAAGTACCTACAGTCAGTGCTACCAGTAGATTTACTTATCACATGGTAAGTGGAATGTCACAGA-----
   ENV GENOMIC HERV-K TAN.   (550) ATTGGTTGGTAGAAGTACCTACTGTCAGTCCCATCTGTAGATTCACTTATCACATGGTAAGCGGGATGTCACTCAGGCCA
      ENV GENOMIC AC025420   (547) ATTGGTTGGTAGAAGTACCTACTGTCAGTCCCATCAGTAGATTCACTTATAACATGGTAAGCGGGATGTCACTCAGGCCA
      ENV GENOMIC AP000776   (550) ACTGGTTGGTAGAAGTACCTATTGTCAGTCCCATCAGTAGATTCACTTATCACATGGTAAGCGGGATGTCACTCAGGCCA
       ENV GENOMIC HERV-K8   (291) --------------------------------------------------------------------------------
       ENV GENOMIC HERV-KI   (550) ATTGGTTAGTAGAAGTACCTACTGTCAGTCCCATCAGTAGATTCACTTATCACATGGTAAGCGGGATGTCACTCAGGCCA
       ENV HERV-K AF023261   (613) ATTGGTTGGTAGAAGTACCTACTGTCAGTCCCATCAGTAGATTCACTTATCACATGGTAAGCGGGATGTCACTCAGGCCA
           ENV GEN AL035086  (336) ATTGGTTGGTAGAAGTACCTACTGTCAGTGCCACCAGTGGATTTACTTATCACAGGGTAAGTGGAATGTCACTCAGGCCA
      ENV GENOMIC AL035587   (550) ACTGGTTGGTAGAAGTACCTACCGTCAGTGCCACCAGTAAATTTACTTATCACATGGTAAGTGGAATGTCACTCGGGCCA
      ENV GENOMIC AC012068   (538) ACTGGTTGGTAGAAGTACCTACTGTCAGTGCCACCAGTAAATTCACTTATCACATGGTAAGTGAAATGTCACTTGGGTCA
      ENV GENOMIC AF277315   (547) ATTGGTTGGTAGAAGTACCTACTGTCATTGCCAGCAATAGATTTACTTATCACATGGTAAGTGAAATGTCACTCGGGCCA
      ENV GENOMIC AF027650   (612) ATTGGTTGGTACAAGTACCTACTGTCAGTACCATCAGTAGATTCACTTATCACATGGTAAGGGGAATGTCACTCAGGCCA
      ENV GENOMIC AC078899   (549) ATTGGTTGGTACAAGTACCTACTGTCAGTACCATCAGTAGATTCACTTATCACATGGTAAGGGGAATGTCACTCAGGCCA
      ENV GENOMIC HERV-KII   (258) ATTGGTTGGTAGAAGTACCTACTGTCAGTCCTAACAGTAGATTCACTTATCACATGGTAAGCGGGATGTCACTCAGGCCA
      ENV GENOMIC AC008813   (570) ATTGGTTGGTAGAAGTACCTACTGTCGGTACCACCAGTAGATTCACTAATCACGCGGTAAGTGGAATGTCACTCAGGCCA
      ENV GENOMIC AC012309   (549) ATTGGTTGGTAGAAGTACTTACTTACTGTACCACCAGTAGATTCACTTATCACATGGTAAGCGGAATGTCACTCAGGCCA
      ENV GENOMIC AL121932   (547) ATTGGTTGGTAAACGTACCTACTTTCAGTACCACCAGTAGATTTACTTATCACATGGTAAGTGGAATGTCACTCAGGCCA
      ENV GENOMIC AD000090   (563) ATTGGTTGGTAGAAGTACCTACTGTCAGTCCCATCAGAAGATTCACTTATCACATGGTAAGCGGGATGTCGCTCAGGCCA
         ENV GEN  AL160008   (429) ATTGGCTAGTTAAGATTCCA------GGTCA--TAATCAAAGACCAGTATCC--------------TGTCATTTA-----
      ENV GENOMIC HEU32496   (441) --------------------------------------------------------------------------------
      ENV GENOMIC AC011467   (314) ATTGGTTGGTAGAAGTACCTACTGTCAGTCCCATCAGTAGATTCACTTATCACATGGTAAGTGGGATGTCACTCAGGCCA
      ENV GENOMIC AF235103   (609) ATTGGTTGGTAGAAGTACCTACTGTCAGTGCTACCAGTAAATTCACTTATCACA-GGTAAGTGAAATGTCACTCGGGTCA
      ENV GENOMIC AC026786   (484) ATTGGTTGGTATAAGTACCTACTGTCAATGCCACCAGTAAATTTACTTATCACATGGTAAGTGGAATGTCAATCGGGTCA
      ENV GENOMIC AC034203   (590) ATTGGTTGGTAGAAGTACCTACTGTCAGTGGCACCAGTAAATTTACTTATCATGTGATAAGTGGAATGTCACTCGGGTCA
      ENV GENOMIC AC018809   (257) ATTGGTTGTTAGAAGTACCTACTGTCAGTCCCATCAGTAGATTCACTTATCACACGGTAAGCAGGATGTCACTCAGGCCA
ENV GENOMIC HERV-K102 AF164610 (310) ATTGGTTGGTAGAAGTACCTACTGTCAGTCCCATCAGTAGATTCACTTATCACATGGTAAGCGGGATGTCACTCAGGCCA
   ENV GENOMIC FRAG. AF260253  (1) --------------------------------------------------------------------------------
                     CONSENSUS (641) ATTGGTTGGTAGAAGTACCTACTGTCAGT CCA CAGTAGATTCACTTATCACATGGTAAG GG ATGTCACTCAGGCCA
```

FIG. 6-9

```
                                         721                                                                            800
         ENV GENOMIC HERV MDA   (609)  ----TAAATAATTTACAGGACCCTTCTTATCAAAGATCATTACAATGTAGGCCTAAGGGGAAGGCTTGCCCCAAGGAAAT
       ENV GENOMIC HERV-K TAN.  (630)  CGGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTTGCCCCAAGGAAAT
         ENV GENOMIC AC025420   (627)  CGGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTTGCCCCAAGGAAAT
         ENV GENOMIC AP000776   (630)  CGGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTTGCCCCAAGGAAAT
          ENV GENOMIC HERV-K8   (291)  --------------------------------------------------------------------------------
          ENV GENOMIC HERV-KI   (630)  CAGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAAGGAAACCTTGCCTCAAGGAAAT
          ENV HERV-K AF023261   (693)  CGGGTAAA------------------------------------------------------------------------
             ENV GEN AL035086   (416)  CAGGTAAATTATTTGCAGGACCCTTCTTATCAAAGATGATTAAAATCTAGGCCTAAGGGGAAGCCTTGCCCCAAAGAAAT
         ENV GENOMIC AL035587   (630)  CAGATAAATAATTTAGAGGACGCTTCTTATCAAAGATCATTAAAATCTGGGCCTAAGGGGAAGCCTTGCCCCAAGGAAAT
         ENV GENOMIC AC012068   (618)  CAAATGAATAATTTACAGGACTCTTCCTATCAAAGATCATTAAGATTTAGGCCTAAGGGAAAATCTTGCCCCAAGGAAAT
         ENV GENOMIC AF277315   (627)  CAGATAAATAATTTACAGGATCCTTCTTATCAAAGATCATTAAAATTTAGGCCTAAGAGGAAGCCTTGCCCCAAGGAAAT
         ENV GENOMIC AF027650   (692)  CGGGTAAA------------------------------------------------------------------------
         ENV GENOMIC AC078899   (629)  TGGGTAAATTATTTACAGGACTTTTCTTATCAAAGGTCATTAAAATTTAGGCCTAAAGGGAAACATTGCCCCAAGGAAAT
         ENV GENOMIC HERV-KII   (338)  CGGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTTGCCCCAAGGAAAT
         ENV GENOMIC AC008813   (650)  CAGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTAGGCCTAAAGGAAAGCCTTACCCCCAA-AAAA
         ENV GENOMIC AC012309   (629)  CAGGTAAATTATTTACAGGACTTTTCTTATCAAAGATCATTAAAATGTAGGCCTAAAGGGAAACCTTGCCCCACGGAAAT
         ENV GENOMIC AL121932   (627)  CAGGTAAATTATTTACAGGACTTTTCTTATCAAAGATCATTAAAATTTAGGCCTAAAGGGAAACCTTGCCCCAAGGAAAT
         ENV GENOMIC AD000090   (643)  CAGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTTGCCCCGAGGAAAT
             ENV GEN  AL160008  (482)  ----------TTTTACAA-AGTTTGGTTCAATTGGAACAGT----TTAAGCCCAGAAAAGAGAGGTGTCAACAAC----C
         ENV GENOMIC HEU32496   (441)  --------------------------------------------------------------------------------
         ENV GENOMIC AC011467   (394)  CGGGTAAATAATTTACAAGACTTTCCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGCAACCTTGCCCCGAGGAAAT
         ENV GENOMIC AF235103   (688)  CAAATAAATAATTTACAGGATTCTTCCTATAAAAGATCATTAAAATTTAGGCTTAAGGGAAAATCTTGCCCCAAGGAAAT
         ENV GENOMIC AC026786   (564)  CAAATGAATAATTTACAGGATTCTTCCTATCAAAGATCATTAAAATTTAGGCCTAAGGGAAAACCATGCCCCAAGGAAAT
         ENV GENOMIC AC034203   (670)  CAAATAAATAATTTACAAAATTCTTCCTATCAAAGATCATTAAAATTTAGGCCTAAAGGGAAACCATGCCCCGAGGAAAT
         ENV GENOMIC AC018809   (337)  CGGGTAAATAATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTTGCCCCAAGAAAAT
ENV GENOMIC HERV-K102 AF164610  (390)  CGGGTAAATTATTTACAAGACTTTTCTTATCAAAGATCATTAAAATTTAGACCTAAAGGGAAACCTTGCCCCAAGGAAAT
    ENV GENOMIC FRAG. AF260253    (1)  --------------------------------------------------------------------------------
                    CONSENSUS   (721)  C GGTAAAT ATTTACA GACTTTTCTTATCAAAGATCATTAAAATTTAG CCTAAAGGGAAACCTTGCCCCAAGGAAAT
```

FIG. 6-10

```
                                 801                                                                          880
      ENV GENOMIC HERV MDA   (685) TCCCAAAGAATCAAAAAGCCCAGAAGTCTTAGTCTGCGGAGAATGTGTGGCTGATACTGCAGTG-TAGTACAAAACAATG
  ENV GENOMIC HERV-K TAN.    (710) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATG
      ENV GENOMIC AC025420   (707) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGTGGTGATATTACAAAACAATG
      ENV GENOMIC AP000776   (710) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATG
       ENV GENOMIC HERV-K8   (291) --------------------------------------------------------------------------------
       ENV GENOMIC HERV-KI   (710) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTAGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATG
       ENV HERV-K AF023261   (701) --------------------------------------------------------------------------------
          ENV GEN AL035086   (496) TCCCAAAGGATCAAAAGGCCCAGAAGTTTTAGTTTGAGAAGAATGTGTGGCTGATAGGACGGTGATATTACAAAACAATG
      ENV GENOMIC AL035587   (710) TCCCAAAGAATCAAAAAGCCCAGAAGCCTTAGTTTGGGAAGAATGTGTGGCTAATACTGCGGTGGTATTACAAAACAATG
      ENV GENOMIC AC012068   (698) TCCAAAAGAATCAAAAGACCCAGAAGTCTTAGTTTGGGAAGAATGTGTGGCTGATACTGCAGTGGTACTACAAAACAATA
      ENV GENOMIC AF277315   (707) TCCCAAAGAATCAAAAGGCCCAGAAGTCTCAGTTTGGGAAGAATGTGTGGCTGATACTGCTGTGGTATTACAAAACAATG
      ENV GENOMIC AF027650   (700) --------------------------------------------------------------------------------
      ENV GENOMIC AC078899   (709) TCCCAAAGGATCAAAAGACATAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAAGAGTGCAGTGATATTACAAAATGATG
      ENV GENOMIC HERV-KII   (418) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATG
      ENV GENOMIC AC008813   (729) TCCCAAAGGATCAAAAGACACAAAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAATGATA
      ENV GENOMIC AC012309   (709) TCCCAAGGTATCAAAAGACACAGAAGTTTTAGTTTAGGAAGAATGTGTGGCCAATAGTGTGGTGATATTACAAAATGATG
      ENV GENOMIC AL121932   (707) TCCCAAAGGATCAAAAGACACAGAAGTTTTAGTTTTGGAAGAATGTGTGGCCAATAGAGCAGTGATATTACAAAACGATG
      ENV GENOMIC AD000090   (723) TTCCAAAGGATCAAAAAATGTAGAAGCTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCAGTGATATTACAAAACAGTG
         ENV GEN  AL160008   (543) TCAATAATGGTCAAAGGATTTAGAAACATTGATTTGGAAGGATTGCATCACTGATCACACTGTGGTACTGCAAAATAATC
      ENV GENOMIC HEU32496   (441) --------------------------------------------------------------------------------
      ENV GENOMIC AC011467   (474) TCCCAAAGGATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTTCAGTAATATTACAAAACAATG
      ENV GENOMIC AF235103   (768) TCCAAAAGAATAAAAAGACTCAGAAGTCTTAGTTTGGGAAGAATGTGTGGCTGATACTGCGGTGGTATTACAAAACAATA
      ENV GENOMIC AC026786   (644) TCCAAAAGAATCAAAAGACCCAGAAGTCTTAGTTTGGGAACAATGTGCGGCTGATACTGCAGTGGTACTACAAAACAATA
      ENV GENOMIC AC034203   (750) TCCAAAAGAATCAAAAGACCCAAAAGTCTTAGTTTAGGAAGAATGTGTGGCTGATACTGCAGTGGTACTACAAAACAATA
      ENV GENOMIC AC018809   (417) TCCCAAAGGATCAAAAAATACAGAAGCTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTAATATTACAAAACAATG
ENV GENOMIC HERV-K102 AF164610 (470) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATG
   ENV GENOMIC FRAG. AF260253  (1) --------------------------------------------------------------------------------
                     CONSENSUS (801) TCCCAAAG ATCAAAA A  CAGAAGTTTTAGTTTGGGAAGAATGTGTGGC AATAGTGC GTGATATTACAAAACAATG
```

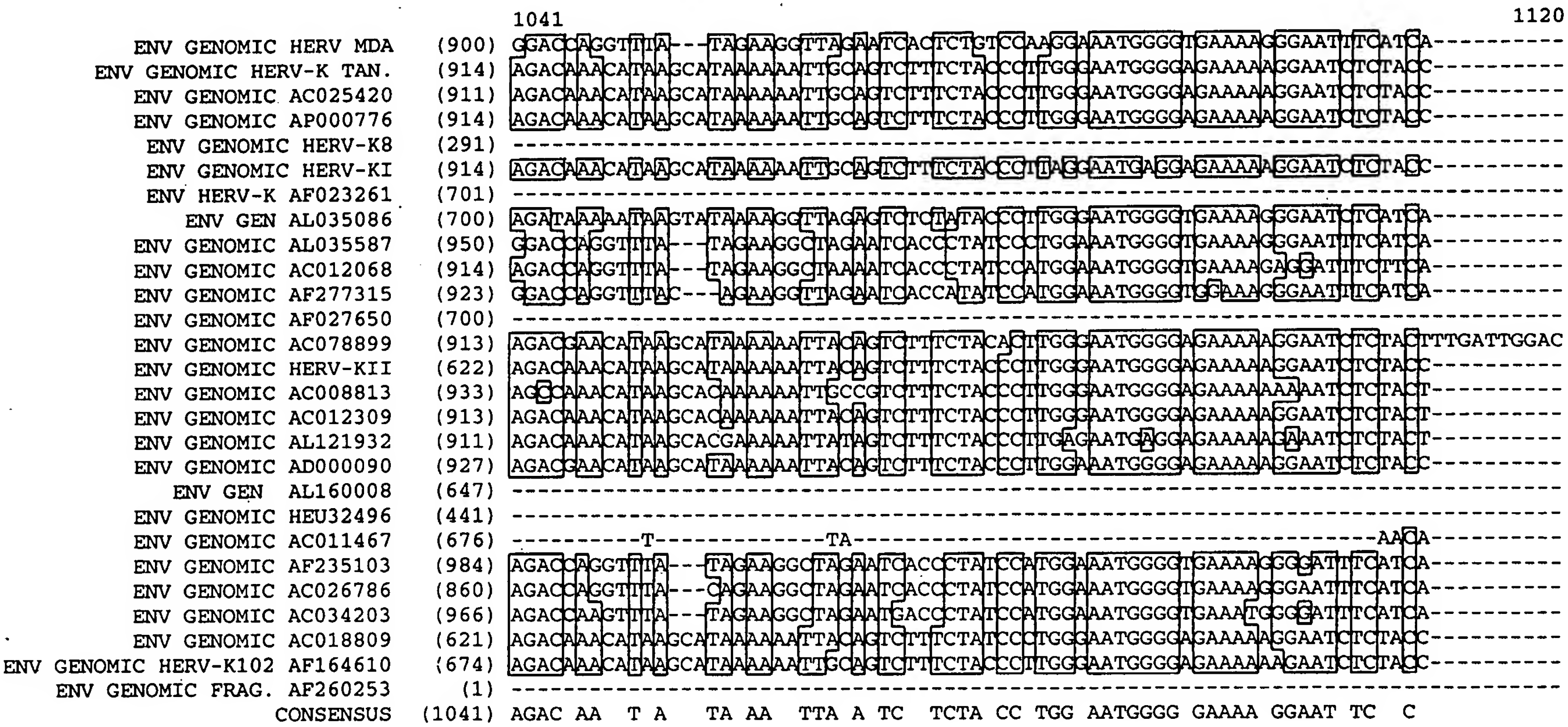
FIG. 6-11

```
                                         881                                                                            960
      ENV GENOMIC HERV MDA  (764) AATTTTGAACTATGATAGACTGGGTCCCTTGAGGCCAATTATATCATA------------------------ACTGTACA
   ENV GENOMIC HERV-K TAN.  (790) AATTCGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACA------------------------ATTGCTCA
      ENV GENOMIC AC025420  (787) AATTTGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACA------------------------ATTGCTCA
      ENV GENOMIC AP000776  (790) AATTTGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACA------------------------ATTGCTCA
       ENV GENOMIC HERV-K8  (291) --------------------------------------------------------------------------------
       ENV GENOMIC HERV-KI  (790) AATTCGGAACTATTATAGATTAGGCACCTCGAGGTCAATTCTACCACA------------------------ATTGCTCA
       ENV HERV-K AF023261  (701) --------------------------------------------------------------------------------
          ENV GEN AL035086  (576) AATTCGGAACCATTATAGATTGGGCACCTCGAGGTCAATTCTACTGCA------------------------ATTGCACA
      ENV GENOMIC AL035587  (790) AATTTGGAACTACTATAATATTATATAATAGTTATATATTATATTATATTATATACAATTATATTATATATAATTGTATG
      ENV GENOMIC AC012068  (778) AATTTGGAACTATTATAGACTAGGCCCCTCGAGGCCAATTATATTATG------------------------ACCGTATG
      ENV GENOMIC AF277315  (787) AATTTGGAACTATTATAGACTGGGCCCCTCAAGGCCAATTATATTATG------------------------ATTGTACA
      ENV GENOMIC AF027650  (700) --------------------------------------------------------------------------------
      ENV GENOMIC AC078899  (789) AATTCAGAACTATTATAGATTGGGCAACTCAAGGTCAATTCTAACACA------------------------ATTGCACA
      ENV GENOMIC HERV-KII  (498) AATTCGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACA------------------------ATTGCTCA
      ENV GENOMIC AC008813  (809) AATTCGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACA------------------------ATTGCACA
      ENV GENOMIC AC012309  (789) AATTTGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACA------------------------ATTGCACA
      ENV GENOMIC AL121932  (787) AATTTGGAACTGTTATAGATAGGGCACCTCGAGGTCAATTCTACCACA------------------------ATTGCACA
      ENV GENOMIC AD000090  (803) AATTCCGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACA------------------------ATTGCACA
          ENV GEN  AL160008  (623) CCTATGGAATCATCATTGATTGGG--------------------------------------------------------
      ENV GENOMIC HEU32496  (441) --------------------------------------------------------------------------------
      ENV GENOMIC AC011467  (554) AATTCAGAACTATTATAGATTGGACATCTGGAGGTCAATTCTACCACA------------------------ATTGCTCA
      ENV GENOMIC AF235103  (848) AATTTGGAACTATTATAAACTGGGCCGCTTGAGGCCAATTATATTATG------------------------ATAGTACA
      ENV GENOMIC AC026786  (724) AATTTGGAACTATTATAGACTGGGCCCCTCGAGGCCAATTATATTATG------------------------ATTGTACG
      ENV GENOMIC AC034203  (830) AGTTTGGAACTATTATAGACTGGGCCCCTCGAGGCCAGTTATATTATG------------------------ATTGTATG
      ENV GENOMIC AC018809  (497) AATTTGGAACTATTATAGATTGGGCACCTTGAGGTCAATTCTACCACA------------------------ATTGCTCA
ENV GENOMIC HERV-K102 AF164610  (550) AATTTGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTACCACA------------------------ATTGCTCA
  ENV GENOMIC FRAG. AF260253    (1) --------------------------------------------------------------------------------
                 CONSENSUS  (881) AATTTGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTA CACA                        ATTGC CA
```

FIG. 6-12

```
                                           961                                                                            1040
           ENV GENOMIC HERV MDA    (820)  GGCCAGACTCATTCATGTTCACAGGCCCCATCCATCTGGCCCATTAATCCAGCCTATGACGGTGATGTAACTGAAAGGCT
      ENV GENOMIC HERV-K TAN.      (846)  GGACAAACTCAGTCGTGTCCAAGTGCACAAG------TG------AGTCCAGCTGTTGATAGCGACTTAACAGAAAGTTT
           ENV GENOMIC AC025420    (843)  GGACAAACTCAGTCGTGTCCAAGTGCACAAG------TG------AGTCCAGCTGTTGATAGTGACTTAACAGAAAGTTT
           ENV GENOMIC AP000776    (846)  GGACAAACTCAGTCGTGTCCAAGTGCACAAG------TG------AGTCCAGCTGTTGATAGCGACTTAACAGAAAGTTT
            ENV GENOMIC HERV-K8    (291)  --------------------------------------------------------------------------------
            ENV GENOMIC HERV-KI    (846)  GGACAAACTCAGCCGTGTCCAAGTGCACAAG------TG------AGTCCAGCTGTTGATAGCGACTTAACAGAAAGTTT
            ENV HERV-K AF023261    (701)  --------------------------------------------------------------------------------
               ENV GEN AL035086    (632)  GGACAAACTCAATCGTGTCCCAGTGCACATG------TG------AGTCCAACTGTGGACAGTGACTTAACAGAAGGTTT
           ENV GENOMIC AL035587    (870)  GGCCAGACTCACTCATGTTTACAGGCCCCATCCATCTGGCCCATTAATCCGGCCTATGATAGTGATTTAATTGAAAGGCT
           ENV GENOMIC AC012068    (834)  GGCCAGACCCACTCATGTTCACAGGCTCCATCTGTCTGGCCCGCTAATCCAGTCTATGATAGTGATTTAACTAAAAGGCT
           ENV GENOMIC AF277315    (843)  GGCCAGACTCACTGATGTTCACAGGCCCCATCCATCTGGCCCACTAATCCGGCCTATGATAGTGATTTAACTGAAAGGCT
           ENV GENOMIC AF027650    (700)  --------------------------------------------------------------------------------
           ENV GENOMIC AC078899    (845)  GGACAAACTCAATCATGTCCCAGTGCACAAG------------TGAGTCCAGCTGTTGATAGTGACTTAACAGGAAGTTT
           ENV GENOMIC HERV-KII    (554)  GGACAAACTCAGTCGTGTCCAAGTGCACAAG------------TGAGTCCAGCTGTTGATAGCGACTTAACAGAAAGTCT
           ENV GENOMIC AC008813    (865)  GGACAAACTCAGTCATGTCCCAGTGCAGAAG------------TGAGTCCAGCTGTTAACAGTGACTTAACAAAAAGTTT
           ENV GENOMIC AC012309    (845)  GGACAAACTCAGTCATGTCCCAGTGCACAAG------TG------AGTCCAACTGTTGATAGTGACTTAACAGAAAGTTT
           ENV GENOMIC AL121932    (843)  GGACAAACTCAATCATGTCCCAGTGCACAAG------------TGAGTCCAGATGTTGATAGCGACATAACAGAAAGTCT
           ENV GENOMIC AD000090    (859)  GGACAAACTCAGTCGTGTCCCAGTGCACAAG------------TGAGTCCAACTGTTGATAGCGACTTCATAGAAAGTTT
               ENV GEN  AL160008   (647)  --------------------------------------------------------------------------------
           ENV GENOMIC HEU32496    (441)  --------------------------------------------------------------------------------
           ENV GENOMIC AC011467    (610)  GGGCAAACTCAGTCGTGACCCAGTGCACAAG------------TGAGTCCAGCTGTTGATAGCGACTTAACAGAAAGT--
           ENV GENOMIC AF235103    (904)  GGCCAGACCCACTCATGTTCACAGGCTCCATCAGTCTGGCCCACTAATCCGGCCTATGATAGTGATTTAACTAAAAGGCT
           ENV GENOMIC AC026786    (780)  GGCCAGGCCCACTCATGTTCACAGGCTCCATCTCTCTGGCCCACTAATCCGGCCTATGATGGTGATTTAACTAAAAGGCT
           ENV GENOMIC AC034203    (886)  GGCCAGACCCACTCGTGTTCACAGGCTCTATCTGTCTGGCCCCCTAATCCAGCCTATAATAGTGATTTAACTAAAAAACT
           ENV GENOMIC AC018809    (553)  GGGCAAACTCAGTCATGTCCCAGGGCACAAG------------TGAGTCCAGCTGTTGAAAGTGACTTAACAGAAAGTTT
ENV GENOMIC HERV-K102 AF164610    (606)  GGACAAACTCAGTCGTGTCCAAGTGCACAAG------------TGAGTCCAGCTGTTGATAGCGACTTAACAGAAAGTTT
    ENV GENOMIC FRAG. AF260253      (1)  --------------------------------------------------------------------------------
                      CONSENSUS    (961)  GG CAAACTCA TC TGTCC AG GCACAAG              AGTCCAGCTGTTGATAG GACTTAACAGAAAGT T
```

FIG. 6-13



```
                                         1041                                                                           1120
        ENV GENOMIC HERV MDA     (900) GGACCAGGTTTA---TAGAAGGTTAGAATCACTCTGTCCAAGGAAATGGGGTGAAAAGGGAATTTCATCA----------
   ENV GENOMIC HERV-K TAN.       (914) AGACAAACATAAGCATAAAAAATTGCAGTCTTTCTACCCTTGGGAATGGGGAGAAAAAGGAATCTCTACC----------
        ENV GENOMIC AC025420     (911) AGACAAACATAAGCATAAAAAATTGCAGTCTTTCTACCCTTGGGAATGGGGAGAAAAAGGAATCTCTACC----------
        ENV GENOMIC AP000776     (914) AGACAAACATAAGCATAAAAAATTGCAGTCTTTCTACCCTTGGGAATGGGGAGAAAAAGGAATCTCTACC----------
         ENV GENOMIC HERV-K8     (291) --------------------------------------------------------------------------------
         ENV GENOMIC HERV-KI     (914) AGACAAACATAAGCATAAAAAATTGCAGTCTTTCTACCCTTAGGAATGAGGAGAAAAAGGAATCTCTACC----------
         ENV HERV-K AF023261     (701) --------------------------------------------------------------------------------
            ENV GEN AL035086     (700) AGATAAAAATAAGTATAAAAGGTTAGAGTCTCTATACCCTTGGGAATGGGGTGAAAAGGGAATCTCATCA----------
        ENV GENOMIC AL035587     (950) GGACCAGGTTTA---TAGAAGGCTAGAATCACCCTATCCCTGGAAATGGGGTGAAAAGGGAATTTCATCA----------
        ENV GENOMIC AC012068     (914) AGACCAGGTTTA---TAGAAGGCTAAAATCACCCTATCCATGGAAATGGGGTGAAAAGAGGATTTCTTCA----------
        ENV GENOMIC AF277315     (923) GGACCAGGTTTAC---AGAAGGTTAGAATCACCATATCCATGGAAATGGGGTGGAAAGGGAATTTCATCA----------
        ENV GENOMIC AF027650     (700) --------------------------------------------------------------------------------
        ENV GENOMIC AC078899     (913) AGACGAACATAAGCATAAAAAATTACAGTCTTTCTACACTTGGGAATGGGGAGAAAAAGGAATCTCTACTTTGATTGGAC
        ENV GENOMIC HERV-KII     (622) AGACAAACATAAGCATAAAAAATTACAGTCTTTCTACCCTTGGGAATGGGGAGAAAAAGGAATCTCTACC----------
        ENV GENOMIC AC008813     (933) AGCCAAACATAAGCACAAAAAATTGCCGTCTTTCTACCCTTGGGAATGGGGAGAAAAAAAAAATCTCTACT----------
        ENV GENOMIC AC012309     (913) AGACAAACATAAGCACAAAAAATTACAGTCTTTCTACCCTTGGGAATGGGGAGAAAAAGGAATCTCTACT----------
        ENV GENOMIC AL121932     (911) AGACAAACATAAGCACGAAAAATTATAGTCTTTCTACCCTTGAGAATGAGGAGAAAAAGAAATCTCTACT----------
        ENV GENOMIC AD000090     (927) AGACGAACATAAGCATAAAAAATTACAGTCTTTCTACCCTTGGAAATGGGGAGAAAAAGGAATCTCTACC----------
           ENV GEN  AL160008     (647) --------------------------------------------------------------------------------
        ENV GENOMIC HEU32496     (441) --------------------------------------------------------------------------------
        ENV GENOMIC AC011467     (676) ----------T-------------TA----------------------------------------AACA----------
        ENV GENOMIC AF235103     (984) AGACCAGGTTTA---TAGAAGGCTAGAATCACCCTATCCATGGAAATGGGGTGAAAAGGGGATTTCATCA----------
        ENV GENOMIC AC026786     (860) AGACCAGGTTTA---CAGAAGGCTAGAATCACCCTATCCATGGAAATGGGGTGAAAAGGGAATTTCATCA----------
        ENV GENOMIC AC034203     (966) AGACCAAGTTTA---TAGAAGGCTAGAATGACCCTATCCATGGAAATGGGGTGAAATGGGGATTTCATCA----------
        ENV GENOMIC AC018809     (621) AGACAAACATAAGCATAAAAAATTACAGTCTTTCTATCCCTGGGAATGGGGAGAAAAAGGAATCTCTACC----------
ENV GENOMIC HERV-K102 AF164610   (674) AGACAAACATAAGCATAAAAAATTGCAGTCTTTCTACCCTTGGGAATGGGGAGAAAAAAGAATCTCTACC----------
   ENV GENOMIC FRAG. AF260253      (1) --------------------------------------------------------------------------------
                   CONSENSUS    (1041) AGAC AA  T A   TA AA  TTA A TC  TCTA CC TGG AATGGGG GAAAA GGAAT TC  C
```

FIG. 6-14

```
                                         1121                                                                          1200
       ENV GENOMIC HERV MDA    (967) --------------------------------------------------------------------------------
   ENV GENOMIC HERV-K TAN.     (984) --------------------------------------------------------------------------------
       ENV GENOMIC AC025420    (981) --------------------------------------------------------------------------------
       ENV GENOMIC AP000776    (984) --------------------------------------------------------------------------------
        ENV GENOMIC HERV-K8    (291) --------------------------------------------------------------------------------
        ENV GENOMIC HERV-KI    (984) --------------------------------------------------------------------------------
        ENV HERV-K AF023261    (701) --------------------------------------------------------------------------------
           ENV GEN AL035086    (770) --------------------------------------------------------------------------------
       ENV GENOMIC AL035587   (1017) --------------------------------------------------------------------------------
       ENV GENOMIC AC012068    (981) --------------------------------------------------------------------------------
       ENV GENOMIC AF277315    (990) --------------------------------------------------------------------------------
       ENV GENOMIC AF027650    (700) --------------------------------------------------------------------------------
       ENV GENOMIC AC078899    (993) TTCAGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCCTAACTCAGCATTTCCGGGTTCACCTTTCCTGTTCCCA
       ENV GENOMIC HERV-KII    (692) --------------------------------------------------------------------------------
       ENV GENOMIC AC008813   (1003) --------------------------------------------------------------------------------
       ENV GENOMIC AC012309    (983) --------------------------------------------------------------------------------
       ENV GENOMIC AL121932    (981) --------------------------------------------------------------------------------
       ENV GENOMIC AD000090    (997) --------------------------------------------------------------------------------
          ENV GEN  AL160008    (647) --------------------------------------------------------------------------------
       ENV GENOMIC HEU32496    (441) --------------------------------------------------------------------------------
       ENV GENOMIC AC011467    (683) --------------------------------------------------------------------------------
       ENV GENOMIC AF235103   (1051) --------------------------------------------------------------------------------
       ENV GENOMIC AC026786    (927) --------------------------------------------------------------------------------
       ENV GENOMIC AC034203   (1033) --------------------------------------------------------------------------------
       ENV GENOMIC AC018809    (691) --------------------------------------------------------------------------------
ENV GENOMIC HERV-K102 AF164610 (744) --------------------------------------------------------------------------------
   ENV GENOMIC FRAG. AF260253    (1) --------------------------------------------------------------------------------
                      CONSENSUS (1121)
```

FIG. 6-15

```
                                    1201                                                                        1280
        ENV GENOMIC HERV MDA   (967) --------------------------------------------------------------------------------
     ENV GENOMIC HERV-K TAN.   (984) --------------------------------------------------------------------------------
        ENV GENOMIC AC025420   (981) --------------------------------------------------------------------------------
        ENV GENOMIC AP000776   (984) --------------------------------------------------------------------------------
         ENV GENOMIC HERV-K8   (291) --------------------------------------------------------------------------------
         ENV GENOMIC HERV-KI   (984) --------------------------------------------------------------------------------
         ENV HERV-K AF023261   (701) --------------------------------------------------------------------------------
            ENV GEN AL035086   (770) --------------------------------------------------------------------------------
        ENV GENOMIC AL035587  (1017) --------------------------------------------------------------------------------
        ENV GENOMIC AC012068   (981) --------------------------------------------------------------------------------
        ENV GENOMIC AF277315   (990) --------------------------------------------------------------------------------
        ENV GENOMIC AF027650   (700) --------------------------------------------------------------------------------
        ENV GENOMIC AC078899  (1073) CCACCCCGACTAACGCACATGCCCACTAGGGCGTGTCACACTCAGAAGTGTGAAACTCAACCGATCCCGCCCCTACCCCG
        ENV GENOMIC HERV-KII   (692) --------------------------------------------------------------------------------
        ENV GENOMIC AC008813  (1003) --------------------------------------------------------------------------------
        ENV GENOMIC AC012309   (983) --------------------------------------------------------------------------------
        ENV GENOMIC AL121932   (981) --------------------------------------------------------------------------------
        ENV GENOMIC AD000090   (997) --------------------------------------------------------------------------------
           ENV GEN  AL160008   (647) --------------------------------------------------------------------------------
        ENV GENOMIC HEU32496   (441) --------------------------------------------------------------------------------
        ENV GENOMIC AC011467   (683) --------------------------------------------------------------------------------
        ENV GENOMIC AF235103  (1051) --------------------------------------------------------------------------------
        ENV GENOMIC AC026786   (927) --------------------------------------------------------------------------------
        ENV GENOMIC AC034203  (1033) --------------------------------------------------------------------------------
        ENV GENOMIC AC018809   (691) --------------------------------------------------------------------------------
ENV GENOMIC HERV-K102 AF164610 (744) --------------------------------------------------------------------------------
  ENV GENOMIC FRAG. AF260253     (1) --------------------------------------------------------------------------------
                   CONSENSUS  (1201)
```

FIG. 6-16

```
                                          1281                                                                            1360
          ENV GENOMIC HERV MDA    (967) --------------------------------------------------------------------------------
       ENV GENOMIC HERV-K TAN.    (984) --------------------------------------------------------------------------------
          ENV GENOMIC AC025420    (981) --------------------------------------------------------------------------------
          ENV GENOMIC AP000776    (984) --------------------------------------------------------------------------------
           ENV GENOMIC HERV-K8    (291) --------------------------------------------------------------------------------
           ENV GENOMIC HERV-KI    (984) --------------------------------------------------------------------------------
           ENV HERV-K AF023261    (701) --------------------------------------------------------------------------------
              ENV GEN AL035086    (770) --------------------------------------------------------------------------------
          ENV GENOMIC AL035587   (1017) --------------------------------------------------------------------------------
          ENV GENOMIC AC012068    (981) --------------------------------------------------------------------------------
          ENV GENOMIC AF277315    (990) --------------------------------------------------------------------------------
          ENV GENOMIC AF027650    (700) --------------------------------------------------------------------------------
          ENV GENOMIC AC078899   (1153) ACCACTCCTCACCCAGCATCCATAAAAGCGCGCTGCACCTTTCGCACAGCGTGACTTCCCCTGGCGGACCAGTGAACCTC
          ENV GENOMIC HERV-KII    (692) --------------------------------------------------------------------------------
          ENV GENOMIC AC008813   (1003) --------------------------------------------------------------------------------
          ENV GENOMIC AC012309    (983) --------------------------------------------------------------------------------
          ENV GENOMIC AL121932    (981) --------------------------------------------------------------------------------
          ENV GENOMIC AD000090    (997) --------------------------------------------------------------------------------
             ENV GEN  AL160008    (647) --------------------------------------------------------------------------------
          ENV GENOMIC HEU32496    (441) --------------------------------------------------------------------------------
          ENV GENOMIC AC011467    (683) --------------------------------------------------------------------------------
          ENV GENOMIC AF235103   (1051) --------------------------------------------------------------------------------
          ENV GENOMIC AC026786    (927) --------------------------------------------------------------------------------
          ENV GENOMIC AC034203   (1033) --------------------------------------------------------------------------------
          ENV GENOMIC AC018809    (691) --------------------------------------------------------------------------------
ENV GENOMIC HERV-K102 AF164610    (744) --------------------------------------------------------------------------------
    ENV GENOMIC FRAG. AF260253      (1) --------------------------------------------------------------------------------
                     CONSENSUS   (1281)
```

FIG. 6-17

```
                                   1361                                                                          1440
      ENV GENOMIC HERV MDA   (967) --------------------------------------------------------------------------------
   ENV GENOMIC HERV-K TAN.   (984) --------------------------------------------------------------------------------
      ENV GENOMIC AC025420   (981) --------------------------------------------------------------------------------
      ENV GENOMIC AP000776   (984) --------------------------------------------------------------------------------
       ENV GENOMIC HERV-K8   (291) --------------------------------------------------------------------------------
       ENV GENOMIC HERV-KI   (984) --------------------------------------------------------------------------------
       ENV HERV-K AF023261   (701) --------------------------------------------------------------------------------
          ENV GEN AL035086   (770) --------------------------------------------------------------------------------
      ENV GENOMIC AL035587  (1017) --------------------------------------------------------------------------------
      ENV GENOMIC AC012068   (981) --------------------------------------------------------------------------------
      ENV GENOMIC AF277315   (990) --------------------------------------------------------------------------------
      ENV GENOMIC AF027650   (700) --------------------------------------------------------------------------------
      ENV GENOMIC AC078899  (1233) ACCGGAGAGCTCAATAAAGAAGATTTTTGCCCTCTTTGTCTTGCCTCTTGGCCTTATTGATCCACGGTGCCTTTCCATTG
      ENV GENOMIC HERV-KII   (692) --------------------------------------------------------------------------------
      ENV GENOMIC AC008813  (1003) --------------------------------------------------------------------------------
      ENV GENOMIC AC012309   (983) --------------------------------------------------------------------------------
      ENV GENOMIC AL121932   (981) --------------------------------------------------------------------------------
      ENV GENOMIC AD000090   (997) --------------------------------------------------------------------------------
         ENV GEN  AL160008   (647) --------------------------------------------------------------------------------
      ENV GENOMIC HEU32496   (441) --------------------------------------------------------------------------------
      ENV GENOMIC AC011467   (683) --------------------------------------------------------------------------------
      ENV GENOMIC AF235103  (1051) --------------------------------------------------------------------------------
      ENV GENOMIC AC026786   (927) --------------------------------------------------------------------------------
      ENV GENOMIC AC034203  (1033) --------------------------------------------------------------------------------
      ENV GENOMIC AC018809   (691) --------------------------------------------------------------------------------
ENV GENOMIC HERV-K102 AF164610   (744) --------------------------------------------------------------------------------
    ENV GENOMIC FRAG. AF260253     (1) --------------------------------------------------------------------------------
                 CONSENSUS  (1361)
```

FIG. 6-18

```
                                       1441                                                                          1520
          ENV GENOMIC HERV MDA    (967) -----------CCTTGACCAAA----GTTAGTCCTGTTACTGGTCCTGAACATCCAGAATTA-GGAAGCTTACTGTGGCC
      ENV GENOMIC HERV-K TAN.     (984) -----------CCAAGACCAAAAATAGTAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTTACTGTGGCC
          ENV GENOMIC AC025420    (981) -----------CCAAGACCAAAAATAATAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTTACTGTGGCC
          ENV GENOMIC AP000776    (984) -----------CCAAGACCAAAAATAGTAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTTACTGTGGCC
           ENV GENOMIC HERV-K8    (291) --------------------------------------------------------------------------------
           ENV GENOMIC HERV-KI    (984) -----------CCAAGACCAAAAATAATAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTTACTGTGGCC
           ENV HERV-K AF023261    (701) --------------------------------------------------------------------------------
              ENV GEN AL035086    (770) -----------CCTCGACCAAAGTTAGTTAGTCCTGTTACTGGTCCTAAGCGTCCGGAACTTTGGAAGCTTACTGTGGCC
          ENV GENOMIC AL035587   (1017) -----------CCTCGACCAAAGTTAGTTAGTCCTGTTACTGGTCCTAAACATCCAAAATTATGGAAGCTTACTGTGGCC
          ENV GENOMIC AC012068    (981) -----------CCCCGACCAAA----GTTAGTCCTGTTGTTGGTCCTGAACACCCAGAATTATGGAAGCTCACTGTGGCC
          ENV GENOMIC AF277315    (990) -----------CTTCGAACAAAGTTAGTTAGTCCTGTTGTTGGTCGTGAACACCCAGAATTATGGAAGCTTACTGTGGCC
          ENV GENOMIC AF027650    (700) --------------------------------------------------------------------------------
          ENV GENOMIC AC078899   (1313) CCTTTCATACTCCAAGACCAAAAATAATAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTACAGAGGCTTACTGTAGCC
          ENV GENOMIC HERV-KII    (692) -----------CCAAGACCAGAAATAATAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTT----TGGCC
          ENV GENOMIC AC008813   (1003) -----------CCAAGAACAAAGATAATAAGTTCTGTTTCTGGTCCTGAACATCCAAAATTATAGAGTCTTACTGTGGCC
          ENV GENOMIC AC012309    (983) -----------CCAAGACCAAAAATAATAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTTACTGTGGCC
          ENV GENOMIC AL121932    (981) -----------CCAAGACCAAAAATAATAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTTAATGTGGCC
          ENV GENOMIC AD000090    (997) -----------CCATGACCAAAAATAATAAGTCCTGTTTCTGGTCCTGAACATCCAGAATGGTGGAGGCTTAGTGTAGCC
              ENV GEN  AL160008   (647) --------------------------------------------------------------------------------
          ENV GENOMIC HEU32496    (441) --------------------------------------------------------------------------------
          ENV GENOMIC AC011467    (683) ------------------------------------TTTCTGGTCATGAACATCCAAAATTATGGAGGCTTACTGTAGCC
          ENV GENOMIC AF235103   (1051) -----------CCCCGCCCAAAGTTAGTTAGTCCTGTTGTTGCTCCTGAACACCCAGAATTATGGAAGCTCACTGTGGCC
          ENV GENOMIC AC026786    (927) -----------CCCCGACCAAAGTTAGTTAGTCCTGTTGTTGGTCCTGAACACCCAAAATTATGGAAGCTCACTGTGGTC
          ENV GENOMIC AC034203   (1033) -----------CCCCGACCAAAGTTAGTTAGTCCTGTTGTTGTTCCTGAACACCCAGAATTATGGAAGCTTACTGTGGCC
          ENV GENOMIC AC018809    (691) -----------CCAAGACCAAAAATAATAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTTACTGTAGCC
ENV GENOMIC HERV-K102 AF164610    (744) -----------CCAAGACCAAAAATAGTAAGTCCTGTTTCTGGTCCTGAACATCCAGAATTATGGAGGCTTACTGTGGCC
    ENV GENOMIC FRAG. AF260253      (1) --------------------------------------------------------------------------------
                     CONSENSUS   (1441)            CC  GACCAAA  TA T AGTCCTGTT CTGGTCCTGAACATCCAGAATTATGGA GCTTACTGTGGCC
```

FIG. 6-19

```
                                          1521                                                                            1600
           ENV GENOMIC HERV MDA   (1031)  TCAC-ACCACATTAGAATTTGTTCTGGAAATCAAGCTATAGGAACAAGAGATCGTAAGTCATATTATACTATCAACCTAA
       ENV GENOMIC HERV-K TAN.   (1053)  TCAC-ACCACATTAGAATTTGGTCTGGAAATCAAACTTTAGAAACAAGAGATCGTAAGCCATTTTATACTATTGACCTGA
           ENV GENOMIC AC025420   (1050)  TCAC-ACCACATTAGAATTTGGTCTGGAAATCAAACTTTAGAAACAAGAGATCGTAAGCCATTTTATACTGTTGACCTAA
           ENV GENOMIC AP000776   (1053)  TCAC-ACCACATTAGAATTTGGTCTGGAAATCAAACTTTAGAAACAAGAGATCGTAAGCCATTTTATACTGTCGACCTAA
            ENV GENOMIC HERV-K8   (291)   --------------------------------------------------------------------------------
            ENV GENOMIC HERV-KI   (1053)  TCAC-ACCACATTAGAATTTGGTCTGGAAATCAAACTTTAGAAACAAGAGATCATAAGCCATTTTATACTATCGACCTAA
            ENV HERV-K AF023261   (701)   --------------------------------------------------------------------------------
               ENV GEN AL035086   (839)   TCGC-ACCACATTAGAATTTGGTCTGGAAATTAAGCTATAAAAACAAGAGATGGTAAGCCATCTTATACTATCGACCTAA
           ENV GENOMIC AL035587   (1086)  TCGC-ACTACATTAGAATTTGGTCTGGAAATCAAGCTACAGAAACAAGAAATCGTAAGCCATATTATACTATCAACCTAA
           ENV GENOMIC AC012068   (1046)  TCGT-ACCACATTAGAATTTGGTCTGGAAATCAAGTTATGGGAACAAGAAATCATAAGCCATATTATACTATTTAACCTAA
           ENV GENOMIC AF277315   (1059)  TCGC-ACCACATTAGAATTTGGTTTGGAAATGAAGCTATAGGAACAAGAGATCGTAAGCCATATTATACTATTTAACCTAA
           ENV GENOMIC AF027650   (700)   --------------------------------------------------------------------------------
           ENV GENOMIC AC078899   (1393)  TCAT-ACCACATTAGAATTTGGTCTGGAAATCAAACTGTAGAAACAAGAGATCGTAAGCCATTTTATACTATCGACCTAA
            ENV GENOMIC HERV-KII   (757)   TGAC-ACCACATTAGAATTTGGTCTGGAAATCAAACTTTAGAAACAAGAGATCGTAAGCCATTTTATACTATCGACCTAA
           ENV GENOMIC AC008813   (1072)  TCAT-ACCGCATTAAAATTTGGTCTGGAAATCAAGCTATAGAAACAAGAGATCGTAAGCCATTTTATACTATCGACCTAA
           ENV GENOMIC AC012309   (1052)  TCAT-ACCGCATTAGAATTTGATCTGGAAATCAAGCTATAGAAACAGGAGATCATAAGCCATTTTATACTATCGACCTAA
           ENV GENOMIC AL121932   (1050)  TCATTACCATATTAGAATTTGGTCTAGAAATCAAGCTATAAAAACAAGAGATCATAAGCCGTGTTACACTATCAACCTAA
           ENV GENOMIC AD000090   (1066)  TCAT-ACTACATTAGAATTTGGTCTGGAAATCAAACTTTAGAAACGAGA--TCATAAGCCATTTTATACTATCGACCTAA
              ENV GEN  AL160008   (647)   --------------------------------------------------------------------------------
           ENV GENOMIC HEU32496   (441)   --------------------------------------------------------------------------------
           ENV GENOMIC AC011467   (727)   TCAT-ACCACATTAGGATTTGATCTGGAAATCAAACTTTAGAAACAAGAGATCATAAGCCATTTTATACTATCGATCTAA
           ENV GENOMIC AF235103   (1120)  TCAT-ACCACATTAGAATTTGGTCTGGAAATCAAGTTATGGGAACAAGAAATCATAAACCATATTTTACTATTTAACCTAA
           ENV GENOMIC AC026786   (996)   TCCT-ACCACATTAAAATTTGGTATGGAAATCAAGTTATGGAAACAAGAAATCACAAGCCATATTACACTATTTAACCTAA
           ENV GENOMIC AC034203   (1102)  TCAT-ACCACACTAGAATTTGGTCTGAAAATCAAGTTATGGGAACAAAAAATCATAAGCCATATTATACTCTTTAACCTAA
           ENV GENOMIC AC018809   (760)   TCAT-ACCACATTAGGATTTGGTCTGGAAATCAAACTTTAGAAACAAGAGATCATCAGCCGTTTTATACTATCGACCTAA
 ENV GENOMIC HERV-K102 AF164610   (813)   TCAC-ACCACATTAGAATTTGGTCTGGAAATCAAACTTTAGAAACAAGAGATTTGTAAGCCATTTTATACTATCGACCTAA
      ENV GENOMIC FRAG. AF260253   (1)     --------------------------------------------------------------------------------
                      CONSENSUS   (1521)  TCA  ACCACATTAGAATTTGGTCTGGAAATCAA CT TAGAAACAAGAGATC TAAGCCAT TTATACTATC ACCTAA
```

FIG. 6-20

```
                                        1601                                                                          1680
        ENV GENOMIC HERV MDA  (1110)  ATTCCAGTCTGACAATTCCTTTGCAAAATTGTGTAAAACTCCCTTATATTGCTAGTTGTAGGAAAAACATAGTTATTAAA
    ENV GENOMIC HERV-K TAN.   (1132)  ATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
        ENV GENOMIC AC025420  (1129)  ATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
        ENV GENOMIC AP000776  (1132)  ATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
         ENV GENOMIC HERV-K8   (291)  --------------------------------------------------------------------------------
         ENV GENOMIC HERV-KI  (1132)  ATTCCAGTCTAACACTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
         ENV HERV-K AF023261   (701)  --------------------------------------------------------------------------------
            ENV GEN AL035086   (918)  ATTCCAGTCTGACAATTCCTTTGCAAATTTGTGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAAAA--TAGTTATTAAC
        ENV GENOMIC AL035587  (1165)  ATTCCAATCTGACAATTCCTTTACAAAGTTGTGTAAAACCCCCTTATAT-GCTAGTTATAGAAAACA--TAGTTATTAAA
        ENV GENOMIC AC012068  (1125)  ATTACAATCTGACAATTCCTTTGCAAAGTTAGGTAAAACCCCCTTATAC-GCTAGTTGTAGGAAATA--TAGTTATTAAA
        ENV GENOMIC AF277315  (1138)  ATTCCAATCTGACAATTCCTTTGCAAAGTTGTGTAAGACCCCCTTATAT-GTTAGTTGTAGGAAAAA--TAGTTATTAAA
        ENV GENOMIC AF027650   (700)  --------------------------------------------------------------------------------
        ENV GENOMIC AC078899  (1472)  ATTCCAGTCTAACAGCTCCTTTACAAAGTTGTGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
        ENV GENOMIC HERV-KII   (836)  ATTCCAGTCTAACGGTTCCTTTACAAAGTTGCGTAAAGCCCTCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
        ENV GENOMIC AC008813  (1151)  ATTCCAGTCTAACAGTTCCTTTGCAAAGTTGTGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
        ENV GENOMIC AC012309  (1131)  ATTCAAGTCTAACGGTTTCTTTACAAAGTTGTATAAAGCGCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
        ENV GENOMIC AL121932  (1130)  ATTCCAGTCTAACGGTTCCTTCACAAAGTTGTGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
        ENV GENOMIC AD000090  (1143)  ATTCCAGTCTAACAGTTCCTTTACAAAGCTGTGTAAAGTCCCTTTATAT-GCTAGTTATAGGAAATA--TAGTTATTAAA
           ENV GEN  AL160008   (647)  --------------------------------------------------------------------------------
        ENV GENOMIC HEU32496   (441)  --------------------------------------------------------------------------------
        ENV GENOMIC AC011467   (806)  ATTCCAGTCTAACGGTTCCTTTACAAAGTTTCATAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
        ENV GENOMIC AF235103  (1199)  AATCCAATCCGACAATTCCTTTGCAAAGTTATGTAAAACCCCCTCATAT-GCTAGTTGTAGGAAACA--TAGTTATTAAA
        ENV GENOMIC AC026786  (1075)  ATTCCAATCTGACAATTCCTTTGCAAAGTTGTGTAAAACCCCCTTATAT-GCTAGTTGTAGGAAACA--TAGTTATTAAA
        ENV GENOMIC AC034203  (1181)  ATTCCAATCTGACAATTCCTTTGCAAAGTTGTGTAAAACCCCCTTATAT-GCTAGTTGTAGGAAACA--TAGTTATTAAA
        ENV GENOMIC AC018809   (839)  ATTCCAGTCTAACGGTTCCTTTACAAAGTTGTGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC HERV-K102 AF164610   (892)  ATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
    ENV GENOMIC FRAG. AF260253     (1)  --------------------------------------------------------------------------------
                   CONSENSUS  (1601)  ATTCCAGTCT ACA TTCCTTT CAAAGTTG GTAAAGCCCCCTTATAT GCTAGTTGTAGGAAATA  TAGTTATTAAA
```

FIG. 6-21

```
                                           1681                                                                          1760
       ENV GENOMIC HERV MDA      (1190)  CCTGATTCCCAAACCATA--ATCTGTGAAAATTGTGGAATGTTTACTTGCATTGATTTGACTTTTAATTGGCAGCACCGT
   ENV GENOMIC HERV-K TAN.       (1209)  CCAGACTCCCAGACTATA--ACCTGTGAAAATTGTAGATTGCTTACTTGCATTGATTCAACTTTTAATTGGCAACACCGT
       ENV GENOMIC AC025420      (1206)  CCAGACTCTCAAACTATA--ACCTGTGAAAATTGTAGATTGCTTACTTGCATTGATTCAACTTTTAATTGGCAACACCGT
       ENV GENOMIC AP000776      (1209)  CCAGACTCCCAGACTATA--ACCTGTGAAAATTGTAGATTGCTTACTTGCATTGATTCAACTTTTAATTGGCAACACCGT
        ENV GENOMIC HERV-K8       (291)  --------------------------------------------------------------------------------
        ENV GENOMIC HERV-KI      (1209)  CCAGACTCCCAGACTATA--ACCTGTGAAAATTGTAGATTGCTTACTTGCATTGATTCAACTTTTAATTGGCAACACCGT
        ENV HERV-K AF023261       (701)  --------------------------------------------------------------------------------
           ENV GEN AL035086       (995)  CCAGATTCCCAAACTATA--ACCTGTGAAAATTGTAGATTGTTTACTTGCATTGATTCAACTTTTAATTGGCAGCACTGT
       ENV GENOMIC AL035587      (1242)  CCAGATTCCCAAACTATA--ACCTGTGAAAACTGTAGATTGTTTACTTGCATTGATTTGACTTTTAATTGGCAGCGCCAT
       ENV GENOMIC AC012068      (1202)  CCAGATTCCCAAACTATA--ACCTGTGAAAACTGTAGATTGTTTACTTGCATTGATTCAACTTTCGACTGGCAGCATCAT
       ENV GENOMIC AF277315      (1215)  CCAGATTCCCAAACTATA--ACCTGTGAAAATTGTAGATTGTTTACTTGCATTGATTCGACTTCTGATTGGCAGCACCAT
       ENV GENOMIC AF027650       (700)  --------------------------------------------------------------------------------
       ENV GENOMIC AC078899      (1549)  CCAGACCCCCAAACTATA--ACCTGTGAAAATTGCAGATTGTTTACTAGCATTGATTCAACTTTTAATTGGCAGCACCGT
       ENV GENOMIC HERV-KII       (913)  CCAGACTCCCAAACTATA--ACCTGTGAAAATTGTAGATTGTTTACTTGCATTGATTCAACTTTTAATTGGCGGCACCGT
       ENV GENOMIC AC008813      (1228)  CCAGACTCCC----------------------------------------------------------------------
       ENV GENOMIC AC012309      (1208)  CCAGACTCCCAAACTATATAACCTGTGAAAATTGCAGATTGTTTACTTGCATTGATTCAACTTTCAATTGGCAGCACCGT
       ENV GENOMIC AL121932      (1207)  CCAGACTCCCAAACTATA--ACCTGTGAAAATTGCAGACTGTTTACTTGCATTGATTCGACTTTTAATTGGCAGCACTGT
       ENV GENOMIC AD000090      (1220)  CCAGACTCTCAAACTATA--ACCTGTGAAAACTGCAGATTGTTTACTTGCATTGATTCAACTTTTAATTGGCAACACCGT
          ENV GEN  AL160008       (647)  --------------------------------------------------------------------------------
       ENV GENOMIC HEU32496       (441)  --------------------------------------------------------------------------------
       ENV GENOMIC AC011467       (883)  CCAGACTTTCAAACTATA--ACCTGTGAAAACTGTAGATTGATTACTTACATTGATTCAACTTTTAATTGGCAGCACCGT
       ENV GENOMIC AF235103      (1276)  CCAGATTCCCAAACTATA--ACCTGTGAAAATTGTAGATTGTTTACTTGCATTGATTCAACTTTTGATTGGCAGCATCGT
       ENV GENOMIC AC026786      (1152)  CCAGATGTCCAAACTATA--ACCTGTGAAAATTGTAGATTGTTTACTTGCATTGATTCAACTTTTGATTGGCAGCATCGT
       ENV GENOMIC AC034203      (1258)  CCAGATTCCCAAACTATA--ACCTGTGAAAATTGTAGATTGTTTACTTGCATTGATTCAACTTTTGATTGGCAGCATCGT
       ENV GENOMIC AC018809       (916)  CCAGACTCTCAAACTATA--ACCTGTAAAAA--GTAGATAGTTTACTTGCATTGATTCGACTTTTAATCGGCAGCACCGT
ENV GENOMIC HERV-K102 AF164610    (969)  CCAGACTCCCAGACTATA--ACCTGTGAAAATTGTAGATTGCTTAGTTGCATTGATTCAACTTTTAATTGGCAACACCGT
   ENV GENOMIC FRAG. AF260253       (1)  --------------------------------------------------------------------------------
                     CONSENSUS   (1681)  CCAGA TCCCAAACTATA  ACCTGTGAAAATTGTAGATTGTTTACTTGCATTGATTCAACTTTTAATTGGCAGCACCGT
```

FIG. 6-22

```
                                        1761                                                                          1840
      ENV GENOMIC HERV MDA  (1268) ATTCTACTAGGAAGAGCAAGAGAGGGTGTGTGGATCCTTGTGTCCATGGACCGACCATGGGAGGCTTCGCTATCCATCCA
  ENV GENOMIC HERV-K TAN.   (1287) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCCTCGCCATCCGTCCA
      ENV GENOMIC AC025420  (1284) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCCTCGCCATCCATCCA
      ENV GENOMIC AP000776  (1287) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCCTCACCATCCATCCA
       ENV GENOMIC HERV-K8   (291) --------------------------------------------------------------------------------
       ENV GENOMIC HERV-KI  (1287) ATTCTGCTAGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTAGGAGGCCTCGCCATGCGTCTA
        ENV HERV-K AF023261  (701) --------------------------------------------------------------------------------
           ENV GEN AL035086 (1073) ATTCTACCAGTGAGAGCAAGAGAGGCCATGTGGATCCCTGTGTCCATGGACCAACTGTAGGAGGCTTCGCCATCCATCCA
      ENV GENOMIC AL035587  (1320) ATTCTGCTAGTGAGGGCAAGAGAAGGTGTGCGGATCCCTGTGTCCATGGACCGACAGTGGGAGGCTTCGCCAT-GTTCCA
      ENV GENOMIC AC012068  (1280) ATTCTGTTAGTCAGGGCAAGAGAGGGTATGGGGATCCCTGTGTCCATGGACTGACCGTGGGAGGCTTCTCCATCTGGACA
      ENV GENOMIC AF277315  (1293) ATTCTGCTGGTGAGGGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCTTCCCCATCCGTCCA
      ENV GENOMIC AF027650   (700) --------------------------------------------------------------------------------
      ENV GENOMIC AC078899  (1627) ATTCTGCTAGTGAGAGCAAGAGAAGGTGTGTGGATCCCTGTGTCCATGGACCGACTGCGGGTGGCCTCGCCATCCGTCTG
      ENV GENOMIC HERV-KII   (991) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCTCTGTGTCCGTGGACTGACCGTGGGAGGCCTCGCCATCCATCCA
      ENV GENOMIC AC008813  (1238) --------------------------------------------------------------------------------
      ENV GENOMIC AC012309  (1288) ATTCTGCTAGTGAGAGCAAGGGAAGGCGTGTGGATCCCTGTGTCCATGGACCGACAGTGGGAGGCCTCGCCATCCATCCA
      ENV GENOMIC AL121932  (1285) ATTCTGCTAGTGAGAGCAAGAGAAGGCGTGTGGATCCCCGTGTCCATGCACCGACCGTGGGAGGCCTCGCCATCTGTCCA
      ENV GENOMIC AD000090  (1298) ATTCTGCTGGTGAGAGCAAGGGAAGGCGTGTGGATCCTTGTGTCCATGGACCGACTGTGGGAGGCCTCACCATCCGTTCA
          ENV GEN  AL160008  (647) --------------------------------------------------------------------------------
      ENV GENOMIC HEU32496   (441) --------------------------------------------------------------------------------
      ENV GENOMIC AC011467   (961) ATTCTGCTGGTGAGAGCAAGAGAAGGCGTGTGGATCCCTGTGTCCATGGACCGACCATGGGAGGCCTCGCCATCCATCCA
      ENV GENOMIC AF235103  (1354) ATTCTGTTAGTGAGGGCAAGAGAGGGTGCGAGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCTTCTCCATCCGTACA
      ENV GENOMIC AC026786  (1230) ATTCTGTTAGTGAGGGCAAGAGAGGGTGCGAGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCTTCTCCATCCGTACA
      ENV GENOMIC AC034203  (1336) ATTCTGTTAGTAAGGGCAAGAAAAGGTGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAAGCTT-------------
      ENV GENOMIC AC018809   (992) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCCTCGCCATCCGTCCA
ENV GENOMIC HERV-K102 AF164610 (1047) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCATGGGAGGCCTCACCATCCGTCCA
   ENV GENOMIC FRAG. AF260253  (1) --------------------------------------------------------------------------------
                 CONSENSUS  (1761) ATTCTGCT GTGAGAGCAAGAGA GG GTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGC TC CCATCC TCCA
```

FIG. 6-23

```
                                           1841                                                                        1920
        ENV GENOMIC HERV MDA     (1348)   TATTTTAACGGAAGTATTAAAAGGAATTCTAACTAGATCCAAAAGATTCATTTTTACTTTGATGGCAGTGATTATGGGCC
     ENV GENOMIC HERV-K TAN.     (1367)   TATTTTGACTGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
        ENV GENOMIC AC025420     (1364)   TATTTTGACTGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
        ENV GENOMIC AP000776     (1367)   TATTTTGACTGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
          ENV GENOMIC HERV-K8     (291)   --------------------------------------------------------------------------------
          ENV GENOMIC HERV-KI    (1367)   TATTTTGACTGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATAGGAT
          ENV HERV-K AF023261     (701)   --------------------------------------------------------------------------------
             ENV GEN AL035086    (1153)   TATTTTAACTGAAGTATTAAAAGGAGTTCTAAATAGATCCAAAAGATTCATTTTTACTTTGATTGCGGTGACTACGGGAT
         ENV GENOMIC AL035587    (1399)   TATTTTAACGGAAGTATTAAAAGGAATTCTAACTAGATCCAAAAGAT----TTTTACTTTGATTGCAGTGATTATGGGCC
         ENV GENOMIC AC012068    (1360)   TATCTTAACAGAAGTATTTAAAAGAGTTCTAACTAGATCTGAAACATTCATTTTTACCTTGATTACAGTGATTATGGGTT
         ENV GENOMIC AF277315    (1373)   TATTTTAATGGAAGTATTAAAAGGAGTTCTAACTAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTCATTATGGGTC
         ENV GENOMIC AF027650     (700)   --------------------------------------------------------------------------------
         ENV GENOMIC AC078899    (1707)   TATTTTGACTGAGGTATTAAAAGACATTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGG-
         ENV GENOMIC HERV-KII    (1071)   TATTTTGACTGAAGTATTAAAAGACATTTTAAATAGATCCAAAAGATTCATTTTTACCTTAATTGCAGTGATTATGGGAT
         ENV GENOMIC AC008813    (1238)   --------------------------------------------------------------------------------
         ENV GENOMIC AC012309    (1368)   TATTTTGACTGAAGTATTAAAAGTCATTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
         ENV GENOMIC AL121932    (1365)   TATTTTGACTGAAGTATTAAAAGGCATTTTAAATAGATCCAAAAGATTCGTTTTTACTTTAATTGCAGTG-TTATCGGAT
         ENV GENOMIC AD000090    (1378)   TATTTTGACTGAAGTATTAAAAGGCGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTACAGTGATTATGGGAT
            ENV GEN  AL160008     (647)   --------------------------------------------------------------------------------
         ENV GENOMIC HEU32496     (441)   --------------------------------------------------------------------------------
         ENV GENOMIC AC011467    (1041)   TATTTTGACTGAAGTATTAAAAGGCATTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
         ENV GENOMIC AF235103    (1434)   TATCTTAACAGAAGTATTAAAAGGAGTTCTAACTAGATCTAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGTC
         ENV GENOMIC AC026786    (1310)   TATCTTAACAGAAGTATTAAAAGGAGTTCTAACTAAATCTAAAAGATTCATTTTTACTTTGATTGCAGTGATTATGGGTC
         ENV GENOMIC AC034203    (1403)   --------------------------------------------------------------------------------
         ENV GENOMIC AC018809    (1072)   TATTTTGACTGAA-TATTAAAAGCCATTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTACAGTGCTTATGGGAT
ENV GENOMIC HERV-K102 AF164610   (1127)   TATTTTGACTGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
   ENV GENOMIC FRAG. AF260253       (1)   --------------------------------------------------------------------------------
                    CONSENSUS    (1841)   TATTTT AC GAAGTATTAAAAGG  TT TAA TAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGG
```

FIG. 6-24

```
                                           1921                                                                          2000
       ENV GENOMIC HERV MDA  (1428) TCATTGCAGTCACAGCTACTGCTGCGGCTGCTGGAATTGCTTTACACTCCTCTGTTCAAACTGCAGAATACGTAAATGAT
    ENV GENOMIC HERV-K TAN.  (1447) TAATTGCAGTCACAGCTACGGCTGCTGTAGCAGGAGTTGCATTGCACTCTTCTGTTCAGTCAGTAAACTTTGTTAATGAT
       ENV GENOMIC AC025420  (1444) TAATTGCAGTCACAGCTATGGCTGCTGTAGCAGGAGTTGCATTGCACTCTTTTGTTCAGTCAGTAAACTTTGTTAATGAT
       ENV GENOMIC AP000776  (1447) TAATTGCAGTCACAGCTACGGGTGCTGTAGCAGGAGTTGCATTGCACTCTTCTGTTCAGTCAGTAAACTTTGTTAATGAT
        ENV GENOMIC HERV-K8   (291) --------------------------------------------------------------------------------
        ENV GENOMIC HERV-KI  (1447) TAATTGCAGTCACAGCTACGGCTGCTGTAGCAGAAGTTGCATTGCACTCTTCTGTTCAGTCAGTAAACTTTGTTAATGAT
        ENV HERV-K AF023261   (701) --------------------------------------------------------------------------------
           ENV GEN AL035086  (1233) TAAGTGCAGTCACAGTTATGGCCGCTGTGGCAGGAGTTGCATTGCACTCTTCTGTTCAGACGGTACACTTTGTTAACAAT
       ENV GENOMIC AL035587  (1475) TTATTGCAGTCACAGCTACTGCTGCAGCTGCTGGAATTGCTTTACACTCCTCTGTTCAAACTGCAGAATATGTAAATGAT
       ENV GENOMIC AC012068  (1440) TTATTGCAGTCACAGCTACTGCTGCGGCTGCTGGAATTGCTTTACACTCCTCTGTTCAAACTGCAGAATATGTGAATAAT
       ENV GENOMIC AF277315  (1453) TTGTTGCAGTCACAGCTACTGCTGTGGCTGCTGGAATTGCTTTACACTCCTCTGTTCAAATGGTAAAATATGTAAATAAT
       ENV GENOMIC AF027650   (700) --------------------------------------------------------------------------------
       ENV GENOMIC AC078899  (1786) ------------------------------------TG------------------------------------------
       ENV GENOMIC HERV-KII  (1151) TAATTGCAGTCACAGCTACGGCTGCTGTGGCAGGAGTTGCATTGCACTCTTCTGTTCAGTCGGTAAACTTTGTTAATGAT
       ENV GENOMIC AC008813  (1238) --------------------------------------------------------------------------------
       ENV GENOMIC AC012309  (1448) TAATCGCAGTCACAACTACAGCCGCTGTGGCAGGAGTTGCATTGCACTCTTCTGTTCGGACAGTAAACTTTGTTAATGAT
       ENV GENOMIC AL121932  (1444) TAAGTGCAGTCACAGCTACGGCCGCTGTGGCAGGAGTTGCATTGCACTCTTCTGTTCAGACAGTAAACTTTGTTAACGAT
       ENV GENOMIC AD000090  (1458) TAATTGCAGTCACAGCTATGGCTGCTGTGGCAGGAGTTGCATTGCACTCTTCTGTTCAGTCAGTAAACTTTGTTAATGAT
           ENV GEN  AL160008  (647) --------------------------------------------------------------------------------
       ENV GENOMIC HEU32496   (441) --------------------------------------------------------------------------------
       ENV GENOMIC AC011467  (1121) TAATTGCAGTCACAGCTACGGCTGCTGTGGCAGGAGTTGCGTTGCACTCTTCTGTTCAGTCAGTAAACTTTGTTAATGAT
       ENV GENOMIC AF235103  (1514) TTATTGCAGTCACAGCTGCTGCTAGGGCTGCTGTAATTGCTTTACCCTCCTCTGTTCACACTGCAGAATATGTGAATAAT
       ENV GENOMIC AC026786  (1390) TTATTGCAGTCACAGCTACTGCTGTGGCTGCTGGAATTGCTTTACACTGCTCTGTTCAAACTACAAAATATGTGAATAAT
       ENV GENOMIC AC034203  (1403) --------------------------------------------------------------------------------
       ENV GENOMIC AC018809  (1151) TAATTGCAGTCACAGCTACGGCTGCTGTGGCAGGAGTTGCGGTGCACTCTTCTGTTCAGTCAGTAAACTTTGTTAATGAT
ENV GENOMIC HERV-K102 AF164610 (1207) TAATTGCAGTCACAGCTACGGCTGCTGTAGCAGGAGTTGCATTGCACTCTTCTGTTCAGTCAGTAAACTTTGTTAATGAT
   ENV GENOMIC FRAG. AF260253   (1) --------------------------------------------------------------------------------
                  CONSENSUS  (1921) T ATTGCAGTCACAGCTAC GCTGC G  GC GGA TTGC TT CACTC TCTGTTCA  C G A A T TGT AAT AT
```

FIG. 6-25

```
                                       2001                                                                       2080
      ENV GENOMIC HERV MDA   (1508) TGGCAAAAGAA-TTCCTCAAAATTGTGGAATTCTCAGATCCAA-ATAGATCAAAAATTGGCAAACCAAATTAATGATCTT
   ENV GENOMIC HERV-K TAN.   (1527) TGGCAAAAAAA-TTCTACAAGATTGTGGAATTCACA-ATCTAGTATTGATCAAAAATTGGCAAATCAAATTAATGATCTT
      ENV GENOMIC AC025420   (1524) TGGCAAAAAAA-TTCTACAAGATTGTGGAATTCACA-ATCTAGTATTGATCAAAAATTGGCAAATCAAATTAATGATCTT
      ENV GENOMIC AP000776   (1527) TGGCAAAAAAA-TTCTACAAGATTGTGGAATTCACA-ATCTAGTATTGATCAAAAATTGGCAAATCAAATTAATGATCTT
       ENV GENOMIC HERV-K8    (291) --------------------------------------------------------------------------------
       ENV GENOMIC HERV-KI   (1527) TGGCAAAAAAA-TTCTACAAGATTGTGGAATTCACA-ATCTAGTATTGATCAAAAATTGGCAAATCAAATTAATGATCTT
       ENV HERV-K AF023261    (701) --------------------------------------------------------------------------------
          ENV GEN AL035086   (1313) TGGCAAAAAAAATTCTACAAGATTGTGGAATTCACA-ATCTGGTATTGATCAAAAATTGGCAAATTAGATTAATGATCTT
      ENV GENOMIC AL035587   (1555) TGGCGAAAGAA-TTCCTCAAAATTGTGGAATTCTCAGACCCAA-ATAAATCAAAAATTGGCAAACGAAATTAATGATCTT
      ENV GENOMIC AC012068   (1520) TGGCAAAAGAA-TTCCTCGAAATTGTGGAATTCTCAGACTCAA-ACAGATCAAAAATTGACAAATCAAAGTAATGATCTT
      ENV GENOMIC AF277315   (1533) TGGCAAAAGAA-TTCCTCAAAATTGTGGAATTCTCAGACCCAA-ATAGATCAAAAATTGGCAAACCAAATTAATGACCTT
      ENV GENOMIC AF027650    (700) --------------------------------------------------------------------------------
      ENV GENOMIC AC078899   (1788) --GCAAAAGAA-TTCTACAAGATTGTGGAATTCACA-ATCTGGTATTGATCAAAAATTAGCAAATCAAATTAATGATTTT
      ENV GENOMIC HERV-KII   (1231) TGGCAAAAGAA-TTCTACAAGATTGTGGAATTCACA-ATCTAGTATTGATCAAAAATTGGCAAATCAAATTAATGATCTT
      ENV GENOMIC AC008813   (1238) --------------------------------------------------------------------------------
      ENV GENOMIC AC012309   (1528) TGGCAAAAGAA-TTCTACAAGATGGTGGAATTCACA-ATCTGGTATTGATCAAAAATTGGCAAATCAAATTAATGATCTT
      ENV GENOMIC AL121932   (1524) TGGCAAAAGAATTC------------------------------------------------------------------
      ENV GENOMIC AD000090   (1538) TGGCAAAAAAG-TTCTACAAGATTGTGGAATTCACA-ATCTAGTATTGATCAAAAATTGGCAAACCAAATTAATGATCTT
          ENV GEN  AL160008   (647) --------------------------------------------------------------------------------
      ENV GENOMIC HEU32496    (441) --------------------------------------------------------------------------------
      ENV GENOMIC AC011467   (1201) TGGCAAAAGAA-TTCCACAAGATTGTGGAATTCACA-ATCTGGTATTGATCAAAAATTGGCAAATCAAATTAATGATCTT
      ENV GENOMIC AF235103   (1594) TGGCAAAAGAA-TTCCTCAAAATTGTGGAATTCTCAGACTCAA-ATAGATCAAAAATTGGCAAATCAAATTAATGATCTT
      ENV GENOMIC AC026786   (1470) TGGCAAAAGAA-TTCCTCAAGACTGTGGAATTCTCAGACTCAA-ATAGATCAAAAATTAGCAAATCAAATTAATGATCTT
      ENV GENOMIC AC034203   (1403) --------------------------------------------------------------------------------
      ENV GENOMIC AC018809   (1231) TGGCAAAAAAA-TGCTACAAGATTGTGGAATTCACA-ATCTGGTATTGATCAAAAATTGGCAAATCAAATTAATGATTTT
ENV GENOMIC HERV-K102 AF164610 (1287) TGGCAAAAGAA-TTCTACAAGATTGTGGAATTCACA-ATCTAGTATTGATCAAAAATTGGCAAATCAAATTAATGATCTT
   ENV GENOMIC FRAG. AF260253   (1) --------------------------------------------------------------------------------
                     CONSENSUS (2001) TGGCAAAA AA TTC  CAA ATTGTGGAATTC CA A C    AT GATCAAAAATTGGCAAATCAAATTAATGATCTT
```

FIG. 6-26

```
                                    2081                                                                           2160
        ENV GENOMIC HERV MDA (1586) AGACAAACTGTCATTTGGATGGGAGA--GGCTCATGAGCTTGGAATATCTTTTTCAGTTACGATGTGACTGGAATACATC
    ENV GENOMIC HERV-K TAN.  (1605) AGACAAACTGTCATTTGGATGGGAGACAGACTCATGAGCTTAGAACATCGTTTCCAGTTACAATGTGACTGGAATACGTC
         ENV GENOMIC AC025420 (1602) AGACAAACTGTCATTTGGATGGGAGACAGGCTCATGAGCTTAGAACATCGTTTCCAGTTACAGTGTGACTGGAATACGTC
         ENV GENOMIC AP000776 (1605) AGACAAACTGTCATTTGGATGGGAGACAGACTCATGAGCTTAGAACATCGTTTCCAGTTACAATGTGACTGGAATACGTC
          ENV GENOMIC HERV-K8  (291) --------------------------------------------------------------------------------
          ENV GENOMIC HERV-KI (1605) AAAAAAACTGTCATTTGGATAGGAGACAGACTCATGAGCTTAGAACATCGTTTCACGTTACAATGTGACTGGAATACGTC
          ENV HERV-K AF023261  (701) --------------------------------------------------------------------------------
             ENV GEN AL035086 (1392) AGACAAAATGTCATTTGGATGGGAGATAAGCTCGTGAGCTTGGAACATCATTTTCAGTTACAGTGTGACTGGAATACGTC
         ENV GENOMIC AL035587 (1633) AGACAAACTGTCATTTGGCTGGGAAATAGGCTCATGAGCTTGGAATATCTTTTTCAGTTACAGTGTGACTGGAATATGTC
         ENV GENOMIC AC012068 (1598) AGACAAACTGTCATTTGGATGGGAGATAGGCTCATAAGTTTGGAATATCTTTTTCAGTTACAGTGTGACTGGAATATGTC
         ENV GENOMIC AF277315 (1611) AGACAAACTGTCATTTGGATGCGAGATAGGCTCATGAGCTTGAAATATCTTTTTCAGTTACAGTGTGACTGGAATACGTC
         ENV GENOMIC AF027650  (700) --------------------------------------------------------------------------------
         ENV GENOMIC AC078899 (1864) AGACAAACTGTCATTTGGATGGGAGATAGGCTTATGAGCTTAGAACATCATTTCCAGTTACAGTGTGAATGGAATACTTC
         ENV GENOMIC HERV-KII (1309) AGACAAACTGTCATTTGGATGGGAGACAGACTCATGAGCTTAGAACATTGTTTCCAGTTACAGTGTGACTGGAATACGTC
         ENV GENOMIC AC008813 (1238) --------------------------------------------------------------------------------
         ENV GENOMIC AC012309 (1606) AGAC----TGTCATTTGGATGGGAGATAGGCTCATGAGCTTAGAACATCATTTCCAGTTACAGTGTGACTGGAATACGTC
         ENV GENOMIC AL121932 (1538) --------------------------------------------------------------------------------
         ENV GENOMIC AD000090 (1616) AGACAAACTGTCATTTGGATGGGAGACAGGCTCATGAGCTTAGAACATCGTTTCCAGTTACAGTGTGACTGGAATACGTC
             ENV GEN  AL160008 (647) --------------------------------------------------------------------------------
         ENV GENOMIC HEU32496  (441) --------------------------------------------------------------------------------
         ENV GENOMIC AC011467 (1279) AGACAAACTGTCATTTGGGTGGGAGACAGACTCATGAGCTTAGAACATCATTTCCAGTTACGATGTGACTGGAATATCTC
         ENV GENOMIC AF235103 (1672) AGACAAACTGTCATTTGGATGGGAGATAGGCTCATAAGTTTGGAATATCTTTTTCAGTTACTGTGTGACTACAATACATC
         ENV GENOMIC AC026786 (1548) AGACAAACTGTCATTTGGATGGGAGATAGGCTCATGAGCCTGGAATATCTTTTTCAGTTA--GTGTGACTGGACTACGTC
         ENV GENOMIC AC034203 (1403) --------------------------------------------------------------------------------
         ENV GENOMIC AC018809 (1309) AGACAAACTGTCATTTGGATGGGAGACAGGCTCATGAGCTTAGAACATCGTTTCCAGTTACAATGTGACTGGAATATGTC
ENV GENOMIC HERV-K102 AF164610 (1365) AGACAAACTGTCATTTGGATGGGAGACAGACTCATGAGCTTAGAACATCGTTTCCAGTTACAATGTGACTGGAATACGTC
   ENV GENOMIC FRAG. AF260253    (1) --------------------------------------------------------------------------------
                    CONSENSUS (2081) AGACAAACTGTCATTTGGATGGGAGA AG CTCATGAGCTT GAA ATC TTT CAGTTACA TGTGACTGGAATACGTC
```

FIG. 6-27

```
                                       2161                                                                         2240
          ENV GENOMIC HERV MDA (1664) AGATTTTTGTGTTACACCACAAGCCTATAATGAGTCTGAGCATCACTGGGACATGGTTAGATGCCATCTGCAAGGAGGAG
       ENV GENOMIC HERV-K TAN. (1685) AGATTTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGAG
          ENV GENOMIC AC025420 (1682) AGATTTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGAG
          ENV GENOMIC AP000776 (1685) AGATTTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGAG
           ENV GENOMIC HERV-K8  (291) --------------------------------------------------------------------------------
           ENV GENOMIC HERV-KI (1685) AGATTTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTAGGACATAGTTAGACGCCATCTACAAGGAAGAG
           ENV HERV-K AF023261  (701) --------------------------------------------------------------------------------
              ENV GEN AL035086 (1472) AGATTTTTGTATTACACCCCAAGCCTGTAATGAGTCTGAGCGTCACTGGGACATGGTTAGATGCCATCTACAAGGAAGAG
          ENV GENOMIC AL035587 (1713) AGATTTTTGTATTACACCCCAAGCCTATAATGAGTCTGAGCATCACTGGGACATGGTTAGATGCCATCTACAGGGAAGAG
          ENV GENOMIC AC012068 (1678) AGATTTTTGTATTACACTTCAAGCCTATAATGAATCTAAACATCACTGGGACATGGTTAGATGCCATCTACAAGGAAGAG
          ENV GENOMIC AF277315 (1691) AGATTTTTGTATTACACCCCGAGCCTACAATGAGTCTGAGCATCACTGGGCCATGGTTAGATGCCATCTACAAGGAAGAG
          ENV GENOMIC AF027650  (700) --------------------------------------------------------------------------------
          ENV GENOMIC AC078899 (1944) AGATTTTTGTATTACACCCCGAGTTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAAGGAAAAG
          ENV GENOMIC HERV-KII (1389) AGATTTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGAG
          ENV GENOMIC AC008813 (1238) --------------------------------------------------------------------------------
          ENV GENOMIC AC012309 (1682) AGATTTTTGTATTACACCTGGAGTTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGATGCCGTCTACAGGGAAGAA
          ENV GENOMIC AL121932 (1538) --------------------------------------------------------------------------------
          ENV GENOMIC AD000090 (1696) AGATTTTTGTATTACACCCCAAGTTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGAG
             ENV GEN  AL160008  (647) --------------------------------------------------------------------------------
          ENV GENOMIC HEU32496  (441) --------------------------------------------------------------------------------
          ENV GENOMIC AC011467 (1359) AGATTTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGATGCCATCTACAGGGAGGAG
          ENV GENOMIC AF235103 (1752) AGATTTTTGTATTACACCTCAAGCCTATAATGAATCTGAACATCACTGGGACATGGTTAGATGCCATCTACAAGGAAGAG
          ENV GENOMIC AC026786 (1626) AGATTTTTGTATTACACCTCGAGCCTATAATGAATCTGAACATCACTGGGACATGGTTAAACGCCGTCTACAAGGAAGAG
          ENV GENOMIC AC034203 (1403) --------------------------------------------------------------------------------
          ENV GENOMIC AC018809 (1389) AGATTTTTGTATTACACCCCAAGT-TGTAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGCAAGAG
ENV GENOMIC HERV-K102 AF164610 (1445) AGATTTTTGTATTACACCCCAAATTTATAATGAGTCTGAGCATCACTGGGACATGGTTAGACGCCATCTACAGGGAAGAG
    ENV GENOMIC FRAG. AF260253    (1) ----------------------------------------------------CTGGTAAGAGCTAGTCTACAGGAGAGAG
                     CONSENSUS (2161) AGATTTTTGTATTACACC CAA   TATAATGAGTCTGAGCATCACTGGGACATGGTTAGA GCCATCTACA GGAAGAG
```

FIG. 6-28

```
                                           2241                                                                        2320
                ENV GENOMIC HERV MDA (1744) AAGATAATCTTACTTTAGACATTTCAAAATTAAAAGAATGCCCAGCCAAGAAAAAATTTTTGAGGCATCAAAAGCCCATT
            ENV GENOMIC HERV-K TAN. (1765) AAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAA--------------CAAATTTTCGAAGCATCAAAAGCCCATT
                ENV GENOMIC AC025420 (1762) AAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAA--------------CAAATTTTCGAAGCATCAAAAGCCCATT
                ENV GENOMIC AP000776 (1765) AAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAA--------------CAAATTTTCAAAGCATCAAAAGCCCATT
                 ENV GENOMIC HERV-K8  (291) --------------------------------------------------------------------------------
                 ENV GENOMIC HERV-KI (1765) AAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAA--------------CAAATTTTTGAAGCATCAAAAGCCCATT
                 ENV HERV-K AF023261  (701) --------------------------------------------------------------------------------
                    ENV GEN AL035086 (1552) AAGATAATCTTACTTCAGACATTTCAAAATTAAAAGAA--------------CAAATTTTTGAGGCATCAAAAGCCCATT
                ENV GENOMIC AL035587 (1793) AAGATAATCTTACTTTAGATATTTCAAAATTAAAATAA--------------CAAAATTTTGAGGCATCGAAAGCCCATT
                ENV GENOMIC AC012068 (1758) AAGATAATCTTACTTTAGATATTTCAAAATTGAAAAAA--------------CAAATTTTTGAAACATCAAAAGCCCAGT
                ENV GENOMIC AF277315 (1771) AAGATAATCTTACTTTAGATATTTCAAAATTAAAAGAA--------------CAAATTTTTGAGGCATCAAAAGCCCATT
                ENV GENOMIC AF027650  (700) --------------------------------------------------------------------------------
                ENV GENOMIC AC078899 (2024) AAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAA--------------CAAATTTTTGAAGCATCAAAAGCCCATT
                ENV GENOMIC HERV-KII (1469) AAGATAATCTCACTTTAGACATTTCCAAATTAAAATAA--------------CAAATTTTCGAAGCATCAAAAGCCCATT
                ENV GENOMIC AC008813 (1238) --------------------------------------------------------------------------------
                ENV GENOMIC AC012309 (1762) AAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAA--------------CAAATTTTTGAAGGATCAAAGCC-C-AT
                ENV GENOMIC AL121932 (1538) --------------------------------------------------------------------------------
                ENV GENOMIC AD000090 (1776) AAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAA--------------CAAATTTCCAAAACATCAAAAGCCCATT
                   ENV GEN  AL160008  (647) --------------------------------------------------------------------------------
                ENV GENOMIC HEU32496  (441) --------------------------------------------------------------------------------
                ENV GENOMIC AC011467 (1439) AAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAA--------------CAAATTTTCAAAACATCAAAAGCCCATT
                ENV GENOMIC AF235103 (1832) AAGATAATCTTACTTTAGATATTTCAAAATTGAAAGAA--------------CAAATTTTTAAAACATCCAAAGCCCAGT
                ENV GENOMIC AC026786 (1706) AAGACAATCTTACTTTAGATATTTCCAAATTGAAAGAAC-------------ATTATTTTTGAAACATCAAAACC-CAGT
                ENV GENOMIC AC034203 (1403) --------------------------------------------------------------------------------
                ENV GENOMIC AC018809 (1468) AAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAA--------------CAAATTTTCAAAACATCAAAAGCCCATT
ENV GENOMIC HERV-K102 AF164610 (1525) AAGATAATCTCACTTTAGACATTTCCAAATTAAAAGAA--------------CAAATTTTCGAAGCATCAAAAGCCCATT
      ENV GENOMIC FRAG. AF260253   (29) A----TATCTCACTT-AGACATTCAATAAGTACAA------------------------TTCAAGCATC-AAAGCCCATT
                           CONSENSUS (2241) AAGATAATCT ACTTTAGACATTTC AAATTAAAAGAA              CAAATTTT  AA CATCAAAAGCCCATT
```

FIG. 6-29

```
                                                 2321                                                                          2400
        ENV GENOMIC HERV MDA       (1824) TAAATTTGGTGCCAGGAACGGAGACAATCGTGAAAGCTGCTGATAGCCTCACAAATCTTAAGCCAGTCACTTGGGTTAAA
     ENV GENOMIC HERV-K TAN.       (1831) TAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAG
        ENV GENOMIC AC025420       (1828) TAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAG
        ENV GENOMIC AP000776       (1831) TAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAG
         ENV GENOMIC HERV-K8        (291) --------------------------------------------------------------------------------
         ENV GENOMIC HERV-KI       (1831) TAAATTTAGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTT-----AAG
         ENV HERV-K AF023261        (701) --------------------------------------------------------------------------------
            ENV GEN AL035086       (1618) TAAATTTGGTGCCAGGAACTGAAGCAATTACGGAAGCTACTGATGGCCTCGCAAATCTTAACCCAGTCACTTGGGTTAAA
        ENV GENOMIC AL035587       (1859) TAAATTTGG------GAACTGAGGCAATCGTGAAAGCTACTGATGGCCTCACAAATCTTAACACTGTCACTTGGTTAAAA
        ENV GENOMIC AC012068       (1824) TAAATCTGGTGCCAGAAACTGAGGCAACGGTGAAAGCTGTTGATAGCCTCACAAATCTTAACCCTGTCACTTGGGTTAAA
        ENV GENOMIC AF277315       (1837) TAAATCTGGTGCCAGAAACTGAGGCAATCGTGAAAGCTGCTGATGGCCTCACAAATCTTAATGCCGTCACTTGGGTTAAA
        ENV GENOMIC AF027650        (700) --------------------------------------------------------------------------------
        ENV GENOMIC AC078899       (2090) TAAATTTGGTACCGGGAACTGAGGCAATCATGGGAGTTGCTGACTGCCTCTCAAATCTTAACCCTGTCACTTGGGTTAAG
        ENV GENOMIC HERV-KII       (1535) TAAATTTGATGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAG
        ENV GENOMIC AC008813       (1238) --------------------------------------------------------------------------------
        ENV GENOMIC AC012309       (1826) TAAATTTGGTACCAGGAACTGAGGCAATCATGG-AGTTGCTGATGGTCTCACAAATCTTAACCCTGTCACTTGGGTTAAG
        ENV GENOMIC AL121932       (1538) --------------------------------------------------------------------------------
        ENV GENOMIC AD000090       (1842) TAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGTAAATCTTAACCCTGTCACTTGGGTTAAG
           ENV GEN  AL160008        (647) --------------------------------------------------------------------------------
        ENV GENOMIC HEU32496        (441) --------------------------------------------------------------------------------
        ENV GENOMIC AC011467       (1505) TAAATTTGGTGCCGGGAACTGAGGCAATCGCAGGAGTTGCTGCTGGCCTCTCAAATCTTAACCCTGTCACTTGGGTTAAG
        ENV GENOMIC AF235103       (1898) TAAATTTGGTGCCAGAAACTGAGGCAATGGAAAAAGCTGTTGATAGCCTCACGAATCTTAAACCTGTCACTTGGGTTAAA
        ENV GENOMIC AC026786       (1772) TAAATCTGGTGCCAGAAACTGAGACAATGGTAAAAGCTGTTGATAGCCTCACAAATCTTAACCCTGTCACTTGGGTTAAA
        ENV GENOMIC AC034203       (1403) --------------------------------------------------------------------------------
        ENV GENOMIC AC018809       (1534) TAAATTTGGTGCCAGGAACTGAGGCAATCGCAGGAGTTGCTGATGGCCTCACAAATCTTAACCCTGTCACTTGGGTTAAG
ENV GENOMIC HERV-K102 AF164610     (1591) TAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAG
    ENV GENOMIC FRAG. AF260253       (79) ---AATTGGTGCA--GAACTGAGGCAATGCAGA---GTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAGG
                   CONSENSUS       (2321) TAAATTTGGTGCCAGGAACTGAGGCAAT G    AG TGCTGATGGCCTC CAAATCTTAACCCTGTCACTTGGGTTAA
```

FIG. 6-30

```
                                          2401                                                                          2480
          ENV GENOMIC HERV MDA   (1904) AGCATCAGAAGTTTCACTATTGTAAATTTCATATTAATCCTTGTATGCCTGTTCTGTCTGTTGTT--AGTCTACAGGTGT
       ENV GENOMIC HERV-K TAN.   (1911) ACCATTGGAAGTACTACGATTATAAATCTCATATTAATCCTTGTGTGCCTGTTTTGTCTGTTGTT--AGTCTGCAGGTGT
          ENV GENOMIC AC025420   (1908) ACCATTGGAAGTACTACGATTATAAATCTCATATTAATCCTTGTGTGCCTGTTTTGTCTGTTGTT--AGTCTGCAGGTGT
          ENV GENOMIC AP000776   (1911) ACCATTGGAAGTACTACAATTATAAATCTCATATTAATCCTTGTGTGCCTGTTTTGTCTGTTGTT--AGTCTGCAGGTGT
           ENV GENOMIC HERV-K8    (291) --------------------------------------------------------------------------------
           ENV GENOMIC HERV-KI   (1906) ACCATCGGAAGTACTACAATTATAAATCTCATATTAATCCTTGTGTGCCTGTTTTGTCTGTTGTT--AGTCTGCAGCTGT
           ENV HERV-K AF023261    (701) --------------------------------------------------------------------------------
              ENV GEN AL035086   (1698) ACCATCAGAAGTTCCATTATTATAAATTTCATATTAATCCTTGTGTGCCTGTTCTGTCTGTTGTT--AGTCTGCAGGTGT
          ENV GENOMIC AL035587   (1933) ACCATCAGAAGTTCCACTATTGTAAATTTCATATTAATCCTTGTATGCCTGTTCTGTCTGTTGTT--AGTCCACAGGTGT
          ENV GENOMIC AC012068   (1904) ACCACTGGAAATTCCACTGTTGCAAATTTTGTATTAATTCTTGTACGTCTGTCCTCTCTGTTGTT--AGTCTACAGGTGT
          ENV GENOMIC AF277315   (1917) ACTATCAGAAGTTCCACTATTGTAAATTTCATATTAATCCTTGTATGTCTGTTCTGTCTGTTGTT--AGTCTACAGGTGT
          ENV GENOMIC AF027650    (700) --------------------------------------------------------------------------------
          ENV GENOMIC AC078899   (2170) ACCATCAGAAGTACTACTATTATAAATTTCATATTAATCCTTGTGTGCCTGTTCTGTCTGTTGTT--AGTCTGCAGGTGT
          ENV GENOMIC HERV-KII   (1615) ACCATCGGAAGTACTATGATTATAAATCTCATATTAATCCTTGTGTGCCTGTTTTGTCTGTTGTT--AGTCTGCAGGTGT
          ENV GENOMIC AC008813   (1238) --------------------------------------------------------------------------------
          ENV GENOMIC AC012309   (1905) ACCATCGGAAGTTCTACTATTGTAAATTTCCTATTAATCCTTGTGTGCCTGTTCTGTCTGTTGTT--AGTCTGCAGGTGT
          ENV GENOMIC AL121932   (1538) --------------------------------------------------------------------------------
          ENV GENOMIC AD000090   (1922) ACCATCGGAAGTACTATAATTATAAATTTCATATTAATCCTTGTGTGCCTGTTCTGTCTGTTGTT--AGTCTGCAGGGGT
              ENV GEN  AL160008   (647) --------------------------------------------------------------------------------
          ENV GENOMIC HEU32496    (441) --------------------------------------------------------------------------------
          ENV GENOMIC AC011467   (1585) ACCATTGGAAGTACTACTATTATAAATTTCATATTAATCCTTGTGTGGCTGTTTTGTCTGTTGTT--ACTCTGCAGGTGT
          ENV GENOMIC AF235103   (1978) ACCATTGGAAATTCCACTATTGCAAATTTTGTATTAATCCTTGTATGTCTGTCCTCTCTATTGTT--AGTCTACAGGTGT
          ENV GENOMIC AC026786   (1852) ACCACTGGAAATTCCACTATTACAAATTTTGTATTAATCCTTGTATGTCTGTCCTTTCTATTATT--AGTCTACAGGTGT
          ENV GENOMIC AC034203   (1403) --------------------------------------------------------------------------------
          ENV GENOMIC AC018809   (1614) ACGATTGGAAGTACTACGATTATAAATTTCATATTAATCCTTGTGTGCCTGTTTTGTCTGTTGTTCAAGTCTGCAGGTGT
ENV GENOMIC HERV-K102 AF164610   (1671) ACCATTGGAAGTACTACGATTATAAATCTCATATTAATCCTTGTGTGCCTGTTTTGTCTGTTGTT--AGTCTGCAGGTGT
    ENV GENOMIC FRAG. AF260253    (151) ATCCATCGAAGTAGTACGAT-GTAAATCTCATATTAATCATTGTGTGCCTGTTTTGTCTGTTGTT--GGTCTGCAGGTGT
                     CONSENSUS   (2401) ACCAT  GAAGT C AC ATT TAAAT TCATATTAATCCTTGT TGCCTGTT TGTCTGTTGTT  AGTCT CAGGTGT
```

FIG. 6-31

```
                                             2481                                                                          2560
       ENV GENOMIC HERV MDA   (1982) ATCCAGCAGCTCCAAAGAGACAGCAACCAGCAAGAATGGGCCATAGTGACGATGGTGGTTTTGTCAAAAAGAAAAGGGGG
   ENV GENOMIC HERV-K TAN.   (1989) ACCCAACAGCTCCGAAGAGACAGCGACCATCGAGAACGGGCCATGATGACGATGGCGGTTTTGTCGAAAAGAAAAGGGGG
       ENV GENOMIC AC025420   (1986) ACCCAACAGCTCCGAAGAGACAGCGACCATCGAGAACGGGCCATGATGACGATGGTGGTTTTGTCGAAAAGAAAAGGGGG
       ENV GENOMIC AP000776   (1989) ACCCAACAGCTCTGAAGAGACAGCAACCATCGAGAACGGGCCATGATGACGATGGCGGTTTTGTCAAAAAGAAAAGGGGG
         ENV GENOMIC HERV-K8   (291) --------------------------------------------------------------------------------
         ENV GENOMIC HERV-KI  (1984) ACCCAACAGCTCCGAAGAGACAGCGACCATCGAGAACAGGCCATGATGACGATAGTGGTTTTGTCGAAAAGAAAAGGGGG
         ENV HERV-K AF023261   (701) --------------------------------------------------------------------------------
            ENV GEN AL035086  (1776) ACCCAGCAGCTCCGAAGAGACAGCGACCATCAAGAACGGGCCATGATGACGATGGCAGTTTTGTCAAAAACAAAAGGGAG
        ENV GENOMIC AL035587  (2011) ATCCACCAGCTCCGAAGAGACAGCGACCAGCAAGAACGGGCCATAACGACGATGGCAGTTTTGTCAAA-----AAGGGGG
        ENV GENOMIC AC012068  (1982) ATCCAGCAGCTCCGGAGAGACAGCAACCAGCGAGAACGGGCCATGATGACTATGGCAGTTTTGTCAAAAAGAAAAGGGAC
        ENV GENOMIC AF277315  (1995) ATCCAACAGCTCCGAAGAGACAGTGACCAGCGAAAACGGGCCGTGATGATGATGGTGGTTTTGTCAGAAAGAAAAGGGGG
        ENV GENOMIC AF027650   (700) --------------------------------------------------------------------------------
        ENV GENOMIC AC078899  (2248) ACCCAGCAGCTCCAAAGAGACAGGGACCATCAAGAACGGGCCATGATAACGATGGTGGTTTTGTCAAAAATAAAAGGGGG
        ENV GENOMIC HERV-KII  (1693) ACCCAACAGCTCCGAAGAGACAGCGACCATCGAGAACGGGCCATGATGACGATGGCGGTTTTGTCGAAAAGAAAAGGGGG
        ENV GENOMIC AC008813  (1238) --------------------------------------------------------------------------------
        ENV GENOMIC AC012309  (1983) ACCCAACAGCTCCAAAGAGACAGCGACCATCGAGAACGGGCCATGATGACGATGGCGGTTTTGTCCAAAAGAAAAGGGGG
        ENV GENOMIC AL121932  (1538) --------------------------------------------------------------------------------
        ENV GENOMIC AD000090  (2000) ACCCAACAGCTCCGAAGAGACAGCGACCATCGAGAAAGAGCCATGATGACGATGGCGGTTTTGTTGAAAAGAAAAGGGGG
             ENV GEN  AL160008 (647) --------------------------------------------------------------------------------
        ENV GENOMIC HEU32496   (441) --------------------------------------------------------------------------------
        ENV GENOMIC AC011467  (1663) ACCCAACAGCTCCGAAGAGACAGCGACCATCCAGAA--------------------------------------------
        ENV GENOMIC AF235103  (2056) ATCCAGCAGCTCCGGAGAGACAGCGGCTAGCGAGAACGGACCATGATGATGATGGCGGTTTTGTCAAAAAGAAAAGGGGG
        ENV GENOMIC AC026786  (1930) ATACAACAGCTCCGGAGAGACAGCGACCAGCGAGAACGGGTCATGATGACGATGGCGGTTTTGTCAAAAAGAAAAGGGGG
        ENV GENOMIC AC034203  (1403) --------------------------------------------------------------------------------
        ENV GENOMIC AC018809  (1694) ACCCAACAGCTCTGAAGAGACAGCGACCATCAAGAACGGGCCATGATGATGATGGCAGTTTTGTCGAAAAGAAAAGGGGG
ENV GENOMIC HERV-K102 AF164610 (1749) ACCCAACAGCTCCGAAGAGACAGCGACCATCGAGAACGGGCCATGATGACGATGGCGGTTTTGTCGAAAAGAAAAGGGGG
  ENV GENOMIC FRAG. AF260253   (228) ACCCAACAGCTCGGAAGAGACAGCGACCATCGAGAACGGGCCATGATGACGATGGCGGTTTTGTCGAAAAGAAAAGGGGG
                   CONSENSUS  (2481) A CCA CAGCTCCGAAGAGACAGCGACCA C AGAACGGGCCATGATGACGATGG GGTTTTGTC AAAAGAAAAGGGGG
```

FIG. 6-32

```
                                             2561                                                                          2640
           ENV GENOMIC HERV MDA   (2062)  GGATATGTAAGGAAAAG----AGAGATCAGACTTTCACTGT-GTCTATGTAGAAA-AGGAAGACATAAGAAACTCCATTT
       ENV GENOMIC HERV-K TAN.    (2069)  --AAATGTGGGGAAAAGCAAGAGAGATCAGATTGTTACTGT-GTCTGTGTAGAAAGAAGTAGACATAGGAGACTCCATTT
           ENV GENOMIC AC025420   (2066)  --AAATGTGGGGAAAAGCAAGAGAGATCAGATTGTTACTGT-GTCTGTGTAGAAAGAAGTAGACATAGGAGACTCCATTT
           ENV GENOMIC AP000776   (2069)  --AAATGTGGGGAAAAGCAAGAGAGATCAGATTGTCACTGT-GTCTGTGTAGAAAGAAGTAGACATAGGAGACTCCATTT
            ENV GENOMIC HERV-K8   (291)   --------------------------------------------------------------------------------
            ENV GENOMIC HERV-KI   (2064)  --AAATGTGGGGAAAAGCAAGAGAGATCAGATTGTTACTGT-GTCTGTGTAGAAAGAAGTAGACATAGGAGACTCCATTT
            ENV HERV-K AF023261   (701)   --------------------------------------------------------------------------------
               ENV GEN AL035086   (1856)  ---AATGTGGGGAAAAGAAAGAGAGATCAGATTGTTACTGT-GTCTATGCAGAAA-AGGAAGACATAAGAAATTCCATTT
           ENV GENOMIC AL035587   (2086)  --ATATGTAGGGAAAAG----AGAGATCCGACTGTTACTGT-GTCTACATAGAAA-AGGAAGACATAA------------
           ENV GENOMIC AC012068   (2062)  --ATATGTAGGGAAAAGAAAGAGAGATCAGACTGTTACTGT-GTCTATGTAGAAA-AGAAAGACATAAGAGACTCCATTT
           ENV GENOMIC AF277315   (2075)  --ATATGCAGGCAAGAGAAAGAGAGATCAGACTGTTACTGTTGTCTGTGTAGAAA-AGGAAGACATAAGAAACTCCATTT
           ENV GENOMIC AF027650   (700)   --------------------------------------------------------------------------------
           ENV GENOMIC AC078899   (2328)  --AAGTGTGGGGAAAAGAAAGAGAGATGAGACTGTTACTAT-GTCTATGTAGAAAGAAGTAGACATAAGAGACTCCATTT
           ENV GENOMIC HERV-KII   (1773)  --AAATGTGGGGAAAAGCAAGAGAGATCAGATTGTTACTGT-GTCTGTGTAGAAAGAAGTAGACATAGGAGACTCCATTT
           ENV GENOMIC AC008813   (1238)  --------------------------------------------------------------------------------
           ENV GENOMIC AC012309   (2063)  --AAATG---GGAAAAG----AGAGATCAGACTGTTACCGT-GTCTATGCAGAAATAAGTAGACATAAGAGACTCCGTTT
           ENV GENOMIC AL121932   (1538)  --------------------------------------------------------------------------------
           ENV GENOMIC AD000090   (2080)  AAATATG--GGGAAAAGAAAGAGAGATCAGATTGTTACTGT-GTCTGTGTAGAAAGAAGTAGACACAGGAGACTCCATTT
               ENV GEN  AL160008  (647)   --------------------------------------------------------------------------------
           ENV GENOMIC HEU32496   (441)   --------------------------------------------------------------------------------
           ENV GENOMIC AC011467   (1699)  --------------------------------------------------------------------------------
           ENV GENOMIC AF235103   (2136)  --ATATGTAGGGAAAAGAGAGAGAGATCAGACTGTTACTGT-GTCTATGTAGAAA-GGGAAGACATAAGAGACTCCATTT
           ENV GENOMIC AC026786   (2010)  --AAATGTAGGGAAAAGAAAGAGAGATCAGACTGTCACTGT-GCCTATGTAGAAA-GGGAAGACATAAGAGACTCCATTT
           ENV GENOMIC AC034203   (1403)  --------------------------------------------------------------------------------
           ENV GENOMIC AC018809   (1774)  --AAATGTGGGGAAAAG----AGAGATCAGATTGTTACTGT--GTCGTGTAGAAATAAGTAGACATAGGAGACTCCATTT
ENV GENOMIC HERV-K102 AF164610   (1829)  --AAATGTGGGGAAAAGCAAGAGAGATCAGATTGTTACTGT-GTCTGTGTAGAAAGAAGTAGACATGGGAGACTCCATTT
     ENV GENOMIC FRAG. AF260253   (308)   --AAATGTGGGGAAAAGCAAGAGAGATCAGACTGTTACTGT-GTCTGTGTAGAAAGAAGTAGACATAGGAGACTCCATTT
                      CONSENSUS   (2561)    A ATGT GGGAAAAG  AGAGAGATCAGA TGTTACTGT GTCT TGTAGAAA A G AGACATA GAGACTCCATTT
```

FIG. 6-33

```
                                      2641                                                           2707
          ENV GENOMIC HERV MDA (2136) TGATCTGTACTAA------------------------------------------------------
       ENV GENOMIC HERV-K TAN. (2146) TGTTATGTACTAA------------------------------------------------------
          ENV GENOMIC AC025420 (2143) TGTTATGTACTAA------------------------------------------------------
          ENV GENOMIC AP000776 (2146) TGTTATGTACTAA------------------------------------------------------
           ENV GENOMIC HERV-K8  (291) -------------------------------------------------------------------
           ENV GENOMIC HERV-KI (2141) TGTTATGTACTAA------------------------------------------------------
           ENV HERV-K AF023261  (701) -------------------------------------------------------------------
              ENV GEN AL035086 (1931) TGATCTGTACTAA------------------------------------------------------
          ENV GENOMIC AL035587 (2146) -------------------------------------------------------------------
          ENV GENOMIC AC012068 (2138) TGAAAAAGACCTGTACTTTGAACAATT----------------------------------------
          ENV GENOMIC AF277315 (2152) TGACCTGTA----------------------------------------------------------
          ENV GENOMIC AF027650  (700) -------------------------------------------------------------------
          ENV GENOMIC AC078899 (2405) TGTTCTGTACTAAGAGAAATTCTTCTGCCTTGAGATGCTGTTAA-----------------------
          ENV GENOMIC HERV-KII (1850) TGTTCTGTACTAA------------------------------------------------------
          ENV GENOMIC AC008813 (1238) -------------------------------------------------------------------
          ENV GENOMIC AC012309 (2133) TGTTCTGTACCAAG-----------------------------------------------------
          ENV GENOMIC AL121932 (1538) -------------------------------------------------------------------
          ENV GENOMIC AD000090 (2157) TGTTCTGTACTAA------------------------------------------------------
             ENV GEN  AL160008  (647) -------------------------------------------------------------------
          ENV GENOMIC HEU32496  (441) -------------------------------------------------------------------
          ENV GENOMIC AC011467 (1699) -------------------------------------------------------------------
          ENV GENOMIC AF235103 (2212) TGAAAAAGACCTGTACTTTGAACAATTGCTTTGCTCAGATGTTGTTAATTTGTAGTTTT--------
          ENV GENOMIC AC026786 (2086) TGAAAAAGACCTGTACTTTAAACAATTGCTTTGCTGAGATGTTGTTAATTTGTAGCTTTCCCCAGCC
          ENV GENOMIC AC034203 (1403) -------------------------------------------------------------------
          ENV GENOMIC AC018809 (1846) TGCTCTGTACTAAG-----------------------------------------------------
ENV GENOMIC HERV-K102 AF164610 (1906) TGTTATGTGTTAAGAAAAATTCTT-------------------------------------------
    ENV GENOMIC FRAG. AF260253  (385) TGTTCTGTACTAA------------------------------------------------------
                     CONSENSUS (2641) TG   TGTAC
```

FIG. 6-34

```
                                      1                                                         60
    GI_4185938_EMB_CAA76878.1_   (1) -----MGQTKSKIKSKYASYLSFIKILLKRGGVKVSTKNLIKLFQIIEQFCPWFPEQGTL
    GI_4185942_EMB_CAA76881.1_   (1) -----MGQTKSKIKSKYASYLSFIKILLKRGGVKVSTKNLIKLFQIIEQFCPWFPEQGTL
    GI_4185946_EMB_CAA76884.1_   (1) -----MGQTKSKIKSKYASYLSFIKILLKRGGVKVSTKNLIKLFQIIEQFCPWFPEQGTL
    GI_5931704_EMB_CAB56602.1_   (1) -------MGQTKTKSKYASYLSFIKILLKRGGVRVSTKNLIKLFQTTEQFCPWFPEQGNL
              GAG OF AB047240    (1) -----MGQTKSKTKSKYASYLSFIKILLKRGGVRVSTKNLIKLFQIIEQFCPWFPEQGTL
          TRANSLATION OF ORF99   (1) YKKAGLGQTKSKTKSKYASYLSFIKILLKRGGVRVSTKNLIKLFQIIEQFCPWFPEQGTL
 TRANSLATION OF G226TOP-LINK     (1) ------------------------------------------------------------
 TRANSLATION OF G591TOP-LINK     (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG      (1) -----MGQTKSKTKSKYASYLSFIKILLKRGGVRVSTKNLIKLFQIIEQFCPWFPEQGTL
                  GAG106-135     (1) ------------------------------------------------------------
                  GAG186-215     (1) ------------------------------------------------------------
                    GAG46-75     (1) --------------------------------------------------CPWFPEQGTL
                      PDG-G1     (1) ------------------------------------------------------------
                      PGD-G2     (1) ------------------------------------------------------------
                      PGD-G3     (1) ------------------------------------------------------------
                   CONSENSUS     (1)                                                   CPWFPEQG L

                                      61                                                       120
    GI_4185938_EMB_CAA76878.1_  (56) DLKDWKRIGKELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTEEDSVSVSDAPGSCIIDC
    GI_4185942_EMB_CAA76881.1_  (56) DLKDWKRIGKELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTEEDSVSVSDAPGSCIIDC
    GI_4185946_EMB_CAA76884.1_  (56) DLKDWKRIGKELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTEEDSVSVSDAPGSCIIDC
    GI_5931704_EMB_CAB56602.1_  (54) DLEDWKRIGKELKQAGRKGNIIPLTVWNDWPIIKAALEPFQTEDS-VSVSDAPGSCIIDC
              GAG OF AB047240   (56) DLKDWKRIGEELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTKEDSVSVSDAPGSCVIDC
          TRANSLATION OF ORF99  (61) DLKDWKRIGEELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTKEDSVSVSDAPGSCVIDC
 TRANSLATION OF G226TOP-LINK     (1) ------------------------------------------------------------
 TRANSLATION OF G591TOP-LINK     (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG     (56) DLKDWKRIGEELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTKEDSVSVSDAPGSCVIDC
                  GAG106-135     (1) --------------------------------------------------DAPGSCIIDC
                  GAG186-215     (1) ------------------------------------------------------------
                    GAG46-75    (11) DLKDWKRIGKELKQAGRKGN----------------------------------------
                      PDG-G1     (1) ---DWKRIGKELKQAGRKG-----------------------------------------
                      PGD-G2     (1) ------------------------------------------------------------
                      PGD-G3     (1) ------------------------------------------------------------
                   CONSENSUS    (61) DL DWKRIG ELKQAGRKGN                              DAPGSCIIDC
```

FIG. 7-1

```
                                    121                                                        180
  GI_4185938_EMB_CAA76878.1_  (116) NENTRKKSQKETEGLHCEYVAEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGPELVGPSE
  GI_4185942_EMB_CAA76881.1_  (116) NENTRKKSQKETESLHCEYVAEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGPELVGPSE
  GI_4185946_EMB_CAA76884.1_  (116) NENTRKKSQKETEGLHCEYVAEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGPELVGPSE
  GI_5931704_EMB_CAB56602.1_  (113) NEKTRKKSQKETETLHCEYVAEPLMAQSTQNVDYNQLQEVIYPETLKLEGKGPELVGPLE
             GAG OF AB047240  (116) NEKTGRKSQKETESLHCEYVTEPVMAQSTQNVDYNQLQGVIYPETLKLEGKGPELVGPSE
         TRANSLATION OF ORF99 (121) NEKTGRKSQKETESLHCEYVTEPVMAQSTQNVDYNQLQGVIYPETLKLEGKGPELVGPSE
TRANSLATION OF G226TOP-LINK   (1) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK   (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG (116) NEKTGRKSQKETESLHCEYVTEPVMAQSTQNVDYNQLQGVIYPETLKLEGKGPELVGPSE
                  GAG106-135 (11) NENTRKKSQKETEGLHCEYV----------------------------------------
                  GAG186-215  (1) ------------------------------------------------------------
                    GAG46-75 (31) ------------------------------------------------------------
                      PDG-G1 (17) ------------------------------------------------------------
                      PGD-G2  (1) ------------------------------------------------------------
                      PGD-G3  (1) ------------------------------------------------------------
                   CONSENSUS (121) NE T KKSQKETE LHCEYV

                                    181                                                        240
  GI_4185938_EMB_CAA76878.1_  (176) SKPRGTSPLPAGQVPVTLQPQKQVKENKTQPPVAYQYWPPAELQYRPPPESQYGYPGMPP
  GI_4185942_EMB_CAA76881.1_  (176) SKPRGTSRLPAGQVPVTLQPQTQVKENKTQPPVAYQYWPPAELQYRPPVESQYGYPGMPP
  GI_4185946_EMB_CAA76884.1_  (176) SKPRGTSPLPAGQVPVTLQPQKQVKENKTQPPVAYQYWPPAELQYRPPPESQYGYPGMPP
  GI_5931704_EMB_CAB56602.1_  (173) SKPRGPSPLSAGQVTVTLQPQAQVRENKTQLPVAYQYWPPAELQYRPPPESQYGYLGMPP
             GAG OF AB047240  (176) SKPRGPSPLPAGQVPVTLQPQTQVKENKTQPPVAYQYWPPAELQYLPPPESQYGYPGMPP
         TRANSLATION OF ORF99 (181) SKPRGPSPLPAGQVPVTLQPQTQVKENKTQPPVAYQYWPPAELQYLPPPESQYGYPGMPP
TRANSLATION OF G226TOP-LINK   (1) --------------------------------------------------SQYGYPGMPP
TRANSLATION OF G591TOP-LINK   (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG (176) SKPRGPSPLPAGQVPVTLQPQTQVKENKTQPPVAYQYWPPAELQYLPPPESQYGYPGMPP
                  GAG106-135 (31) ------------------------------------------------------------
                  GAG186-215  (1) ----------AGQVPVTLQPQKQVKENKTQPPVAYQYWPP--------------------
                    GAG46-75 (31) ------------------------------------------------------------
                      PDG-G1 (17) ------------------------------------------------------------
                      PGD-G2  (1) ------------------------------------------------------------
                      PGD-G3  (1) ------------------------------------------------------------
                   CONSENSUS (181)           AGQV VTLQPQ QVKENKTQ PVAYQYWPP          SQYGY GMPP
```

FIG. 7-2

```
                                    241                                                        300
GI_4185938_EMB_CAA76878.1_  (236) APQGRAPYPQPPTRRLNPTAPPSRQGSKLHEIIDKSRKEGDTEAWQFPVTLEPMPPGEGA
GI_4185942_EMB_CAA76881.1_  (236) APQGRAPYPQPPTRRLNPTAPPSRRGSELHEIIDKSRKEGDTEAWQFPVMLEPMPPGEGA
GI_4185946_EMB_CAA76884.1_  (236) APQGRAPYPQPPTRRLNPTAPPSRQGSKLHEIIDKSRKEGDTEAWQFPVTLEPMPPGEGA
GI_5931704_EMB_CAB56602.1_  (233) APQDREPYPQPPTRRQCYGTT---------------------------------------
          GAG OF AB047240  (236) ALQGRAPYPQPPTVRLNPTASRSGQGGTLHAVIDEARKQGDLEAWRFLVILQLVQAGEET
      TRANSLATION OF ORF99  (241) ALQGRAPYPQPPTVRLNPTASRSGQGGTLHAVIDEARKQGDLEAWRFLVILQLVQAGEET
TRANSLATION OF G226TOP-LINK  (11) APQGRAPYPQPPTRRLNPTA----------------------------------------
TRANSLATION OF G591TOP-LINK   (1) ------------------------------------------------------------
  TRANSLATION OF LNCAP-GAG  (236) ALQGRAPYPQPPTVRLNPTASRSGQGGTLHAVIDEARKQGDLEAWRFLVILQLVQAGEET
               GAG106-135   (31) ------------------------------------------------------------
               GAG186-215   (31) ------------------------------------------------------------
                 GAG46-75   (31) ------------------------------------------------------------
                   PDG-G1   (17) ------------------------------------------------------------
                   PGD-G2    (1) --------------------------SKLHEIIDKSRKEGDT------------------
                   PGD-G3    (1) ------------------------------------------------------------
                CONSENSUS  (241) A Q R PYPQPPT R

                                    301                                                        360
GI_4185938_EMB_CAA76878.1_  (296) QEGEPPTVEARYKSFSIKKLKDMKEGVKQYGPNSPYMRTLLDSIAHGHRLIPYDWEILAK
GI_4185942_EMB_CAA76881.1_  (296) QEGEPPTVEARYKSFSIKMLKDMKEGVKQYGPNSPYMRTLLDSIAHGHRLIPYDWEILAK
GI_4185946_EMB_CAA76884.1_  (296) QEGEPPTVEARYKSFSIKKLKDMKEGVKQYGPNSPYMRTLLDSIAHGHRLIPYDWEILAK
GI_5931704_EMB_CAB56602.1_  (254) ------------------------------------------------------------
          GAG OF AB047240  (296) QVGAPARAETRCEPFTMKMLKDIKEGVKQYGSNSPYIRTLLDSIAHGNRLTPYDWESLAK
      TRANSLATION OF ORF99  (301) QVGAPARAETRCEPFTMKMLKDIKEGVKQYGSNSPYIRTLLDSIAHGNRLTPYDWESLAK
TRANSLATION OF G226TOP-LINK  (31) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK   (1) ------------------------------------------------------------
  TRANSLATION OF LNCAP-GAG  (296) QVGAPARAETRCEPFTMKMLKDIKEGVKQYGSNSPYIRTLLDSIAHGNRLTPYDWESLAK
               GAG106-135   (31) ------------------------------------------------------------
               GAG186-215   (31) ------------------------------------------------------------
                 GAG46-75   (31) ------------------------------------------------------------
                   PDG-G1   (17) ------------------------------------------------------------
                   PGD-G2   (17) ------------------------------------------------------------
                   PGD-G3    (1) ------------------------------------------------------------
                CONSENSUS  (301)
```

FIG. 7-3

```
                                    361                                                        420
 GI_4185938_EMB_CAA76878.1_  (356) SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA
 GI_4185942_EMB_CAA76881.1_  (356) SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA
 GI_4185946_EMB_CAA76884.1_  (356) SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA
 GI_5931704_EMB_CAB56602.1_  (254) ------------------------------------------------------------
            GAG OF AB047240  (356) SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA
        TRANSLATION OF ORF99 (361) SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA
TRANSLATION OF G226TOP-LINK   (31) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK    (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG  (356) SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA
                 GAG106-135   (31) ------------------------------------------------------------
                 GAG186-215   (31) ------------------------------------------------------------
                   GAG46-75   (31) ------------------------------------------------------------
                     PDG-G1   (17) ------------------------------------------------------------
                     PGD-G2   (17) ------------------------------------------------------------
                     PGD-G3    (1) ------------------------------------------------------------
                  CONSENSUS  (361)

                                    421                                                        480
 GI_4185938_EMB_CAA76878.1_  (416) IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI
 GI_4185942_EMB_CAA76881.1_  (416) IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIANEKARKVI
 GI_4185946_EMB_CAA76884.1_  (416) IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI
 GI_5931704_EMB_CAB56602.1_  (254) ------------------------------------------------------------
            GAG OF AB047240  (416) IEQVRAICLRAWGKIQDPGTAFP-INSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI
        TRANSLATION OF ORF99 (421) IEQVRAICLRAWGKIQDPGTAF-PINSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI
TRANSLATION OF G226TOP-LINK   (31) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK    (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG  (416) IEQVRAICLRAWGKIQDPGTAFP-INSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI
                 GAG106-135   (31) ------------------------------------------------------------
                 GAG186-215   (31) ------------------------------------------------------------
                   GAG46-75   (31) ------------------------------------------------------------
                     PDG-G1   (17) ------------------------------------------------------------
                     PGD-G2   (17) ------------------------------------------------------------
                     PGD-G3    (1) ------------------------------------------------------------
                  CONSENSUS  (421)
```

FIG. 7-4

```
                                      481                                                        540
GI_4185938_EMB_CAA76878.1_      (476) VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGIGGAMYKAMLMAQAITGVVL
GI_4185942_EMB_CAA76881.1_      (476) VELMAYENPNPECQSAIKPLKGKVPAGSDVISEYVKACDGMGGAMHKAMLMAQAITGVVL
GI_4185946_EMB_CAA76884.1_      (476) VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGIGGAMHKAMLMAQAITGVVL
GI_5931704_EMB_CAB56602.1_      (254) ------------------------------------------------------------
             GAG OF AB047240    (475) VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIGGAMHKAMLMAQAMRGLTL
          TRANSLATION OF ORF99  (480) VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIGGAMHKAMLMAQAMRGLTL
TRANSLATION OF G226TOP-LINK      (31) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK       (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG     (475) VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIGGAMHKAMLMAQAMRGLTL
                GAG106-135       (31) ------------------------------------------------------------
                GAG186-215       (31) ------------------------------------------------------------
                  GAG46-75       (31) ------------------------------------------------------------
                    PDG-G1       (17) ------------------------------------------------------------
                    PGD-G2       (17) ------------------------------------------------------------
                    PGD-G3        (1) ------------------------------------------------------------
                 CONSENSUS      (481)

                                      541                                                        600
GI_4185938_EMB_CAA76878.1_      (536) GGQVRTFGRKCYNCGQIGHLKKNCPVLNKQNITIQATTTG-REPPDLCPRCKKGKHWASQ
GI_4185942_EMB_CAA76881.1_      (536) GGQVRTFGGKCYNCGQIGHLKKNCPVLNKQNITIQATTTG-REPPDLCPRCKKGKHWASQ
GI_4185946_EMB_CAA76884.1_      (536) GGQVRTFGRKCYNCGQIGHLKKNCPVLNKQNITIQATTTG-REPPDLCPRCKKGKHWASQ
GI_5931704_EMB_CAB56602.1_      (254) ------------------------------------------------------------
             GAG OF AB047240    (535) GGQVRTFGKKCYNCGQIGHLKRSCPVLNKQNIINQAITAKNKKPSGLCPKCGKGKHWANQ
          TRANSLATION OF ORF99  (540) GGQVRTFGKKCYNCGQIGHLKRSCPVLNKQNIINQAITAKNKKPSGLCPKCGKGKHWANQ
TRANSLATION OF G226TOP-LINK      (31) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK       (1) --------------------------------------------------------WASQ
   TRANSLATION OF LNCAP-GAG     (535) GGQVRTFGKKCYNCGQIGHLKRSCPVLNKQNIINQAITAKNKKPSGLCPKCGKGKHWANQ
                GAG106-135       (31) ------------------------------------------------------------
                GAG186-215       (31) ------------------------------------------------------------
                  GAG46-75       (31) ------------------------------------------------------------
                    PDG-G1       (17) ------------------------------------------------------------
                    PGD-G2       (17) ------------------------------------------------------------
                    PGD-G3        (1) ------------------------------------------------------------
                 CONSENSUS      (541)
```

FIG. 7-5

```
                                      601                                                        660
 GI_4185938_EMB_CAA76878.1_  (595) CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFPIQPFVPQGFQGQQP-PLSQVFQGISQLPQ
 GI_4185942_EMB_CAA76881.1_  (595) CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFPIQPFVPHGFQGQQP-PLSQVFQGISQLPQ
 GI_4185946_EMB_CAA76884.1_  (595) CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFPIQPFVPQGFQGQQP-PLSQVFQGISQLPQ
 GI_5931704_EMB_CAB56602.1_  (254) ------------------------------------------------------------
            GAG OF AB047240  (595) CHSKFDKDGQPLSGNRKRGQPQAPQQTGAFPVQLFVPQGFQGQQPLQKIPPLQGVSQLQQ
        TRANSLATION OF ORF99 (600) CHSKFDKDGQPLSGNRKRGQPQAPQQTGAFPVQLFVPQGFQGQQPLQKIPPLQGVSQLQQ
TRANSLATION OF G226TOP-LINK  (31) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK   (5) CRSKFDKNGQPLSGNEQRGQPQAPQQ----------------------------------
   TRANSLATION OF LNCAP-GAG  (595) CHSKFDKDGQPLSGNRKRGQPQAPQQTGAFPVQLFVPQGFQGQQPLQKIPPLQGVSQLQQ
                 GAG106-135  (31) ------------------------------------------------------------
                 GAG186-215  (31) ------------------------------------------------------------
                   GAG46-75  (31) ------------------------------------------------------------
                     PDG-G1  (17) ------------------------------------------------------------
                     PGD-G2  (17) ------------------------------------------------------------
                     PGD-G3   (1) CRSKFDKNGQPLSGNE--------------------------------------------
                  CONSENSUS (601) C SKFDK GQPLSGN

                                      661         673
 GI_4185938_EMB_CAA76878.1_  (654) YNNCPPPQAAVQQ
 GI_4185942_EMB_CAA76881.1_  (654) YNNCPPPQAAVQQ
 GI_4185946_EMB_CAA76884.1_  (654) YNNCPPPQAAVQQ
 GI_5931704_EMB_CAB56602.1_  (254) -------------
            GAG OF AB047240  (655) SNSCPAPQQAAPQ
        TRANSLATION OF ORF99 (660) SNSCPAPQQAAPQ
TRANSLATION OF G226TOP-LINK  (31) -------------
TRANSLATION OF G591TOP-LINK  (31) -------------
   TRANSLATION OF LNCAP-GAG  (655) SNSCPAPQQAAPQ
                 GAG106-135  (31) -------------
                 GAG186-215  (31) -------------
                   GAG46-75  (31) -------------
                     PDG-G1  (17) -------------
                     PGD-G2  (17) -------------
                     PGD-G3  (17) -------------
                  CONSENSUS (661)
```

FIG. 7-6

```
                                           1                                                          60
     GI_4185939_EMB_CAA76879.1_      (1) MLTDLRAVN---AVIQPMGPLQPGLPSPAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA
     GI_4185943_EMB_CAA76882.1_      (1) MLTDLRAVNAVNAVIQPMGPLQPGLPSLAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA
     GI_4185947_EMB_CAA76885.1_      (1) MLTDLRAVN---AVIQPMGPLQPGLPSPAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA
     GI_5931705_EMB_CAB56603.1_      (1) -----------------------------MIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA
                ENV OF AB047240      (1) ------------------------------------------------------------
    TRANSLATION OF P386TOP-LINK      (1) ------------------------------------------------------------
     TRANSLATION OF POL349-LINK      (1) ------------------------------------------------------------
           LNCAP-GENOMEA-POLORF      (1) ------------------------------------------------------------
TRANSLATION OF LNCAP-POL-GENA-GOODA  (1) ------------------------------------------------------------
       TRANSLATION OF ORF111-10      (1) ------------------------------------------------------------
                         PGD-P1      (1) ------------------------------------------------------------
                         PGD-P2      (1) ------------------------------------------------------------
                          PGDP3      (1) ------------------------------------------------------------
                      CONSENSUS      (1)

                                         61                                                        120
     GI_4185939_EMB_CAA76879.1_     (58) FTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIHCIDDILC
     GI_4185943_EMB_CAA76882.1_     (61) FTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIHYIDDILC
     GI_4185947_EMB_CAA76885.1_     (58) FTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIHCIDDILC
     GI_5931705_EMB_CAB56603.1_     (32) FTIPAINNKEPATRFQWKVLPQGMLNSPTLCQTFVGRALQPVRDKFSDCYIIHYFDDILC
                ENV OF AB047240      (1) ------------------------------------------------------------
    TRANSLATION OF P386TOP-LINK      (1) ------------------------------------------------------------
     TRANSLATION OF POL349-LINK      (1) ------------------------------------------------------------
           LNCAP-GENOMEA-POLORF      (1) ------------------------------------------------------------
TRANSLATION OF LNCAP-POL-GENA-GOODA  (1) ------------------------------------------------------------
       TRANSLATION OF ORF111-10      (1) ------------------------------------------------------------
                         PGD-P1      (1) ------------------------------------------------------------
                         PGD-P2      (1) ------------------------------------------------------------
                          PGDP3      (1) ------------------------------------------------------------
                      CONSENSUS     (61)
```

FIG. 8-1

```
                                                121                                                        180
          GI_4185939_EMB_CAA76879.1_  (118) AAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDT
          GI_4185943_EMB_CAA76882.1_  (121) AAEMKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLEMQIENRKIKPPKIEIRKDT
          GI_4185947_EMB_CAA76885.1_  (118) AAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDT
          GI_5931705_EMB_CAB56603.1_   (92) AAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDT
                     ENV OF AB047240    (1) ------------------------------------------------------------
         TRANSLATION OF P386TOP-LINK    (1) ------------------------------------------------------------
          TRANSLATION OF POL349-LINK    (1) ------------------------------------------------------------
                LNCAP-GENOMEA-POLORF    (1) ------------------------------------------------------------
TRANSLATION OF LNCAP-POL-GENA-GOODA    (1) ------------------------------------------------------------
            TRANSLATION OF ORF111-10    (1) ------------------------------------------------------------
                              PGD-P1    (1) -------------------------------------------IENRKIKPQKIEIRKD-
                              PGD-P2    (1) ------------------------------------------------------------
                               PGDP3    (1) ------------------------------------------------------------
                           CONSENSUS  (121)

                                                181                                                        240
          GI_4185939_EMB_CAA76879.1_  (178) LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGDSDLNSKRMLTPEATKEIKLVEE
          GI_4185943_EMB_CAA76882.1_  (181) LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGDSDLNSKRMLTPEATKEIKLVEE
          GI_4185947_EMB_CAA76885.1_  (178) LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGDSDLNSKRMLTPEATKEIKLVEE
          GI_5931705_EMB_CAB56603.1_  (152) LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGDSDLNSKRMLTPEATKEIKLVEE
                     ENV OF AB047240    (1) ------------------------------------------------------------
         TRANSLATION OF P386TOP-LINK    (1) ------------------------------------------------------------
          TRANSLATION OF POL349-LINK    (1) ------------------------------------------------------------
                LNCAP-GENOMEA-POLORF    (1) ------------------------------------------------------------
TRANSLATION OF LNCAP-POL-GENA-GOODA    (1) ------------------------------------------------------------
            TRANSLATION OF ORF111-10    (1) ------------------------------------------------------------
                              PGD-P1   (17) ------------------------------------------------------------
                              PGD-P2    (1) ------------------------------------------------------------
                               PGDP3    (1) ------------------------------------------------------------
                           CONSENSUS  (181)
```

FIG. 8-2

```
                                                241                                                        300
          GI_4185939_EMB_CAA76879.1_    (238) KIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQIAT
          GI_4185943_EMB_CAA76882.1_    (241) KIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQMAT
          GI_4185947_EMB_CAA76885.1_    (238) KIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQIAT
          GI_5931705_EMB_CAB56603.1_    (212) KIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQIAT
                     ENV OF AB047240      (1) ---------------------------------------------------------MAT
         TRANSLATION OF P386TOP-LINK      (1) ------------------------------------------------------------
          TRANSLATION OF POL349-LINK      (1) ------------------------------------------------------------
                LNCAP-GENOMEA-POLORF      (1) ----------DHLAPLQILIFGTAHSLTAIIVQNTDLVDWSFLPHSTIKTFTLYLDQMAT
TRANSLATION OF LNCAP-POL-GENA-GOODA      (1) ----------DHLAPLQILIFGTAHSLTAIIVQNTDLVDWSFLPHSTIKTFTLYLDQMAT
           TRANSLATION OF ORF111-10      (1) ----YKKAGSDHLAPLQILIFGTAHSLTAIIVQNTDLVDWSFLPHSTIKTFTLYLDQMAT
                              PGD-P1     (17) ------------------------------------------------------------
                              PGD-P2      (1) ------------------------------------------------------------
                               PGDP3      (1) ------------------------------------------------------------
                           CONSENSUS    (241)           D LAPLQLLIFATAHS TGIIIQNTDLVEWSFLPHSTVKTFTLYLDQMAT

                                                301                                                        360
          GI_4185939_EMB_CAA76879.1_    (298) LIGQTRLRIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWKIGLANFVGIIDNHYPKTKIF
          GI_4185943_EMB_CAA76882.1_    (301) LIGQTRLRIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWQIGLANFVGIIDNHYPKTKIF
          GI_4185947_EMB_CAA76885.1_    (298) LIGQTRLRIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWKIGLANFVGIIDNHYPKTKIF
          GI_5931705_EMB_CAB56603.1_    (272) LIGPTRLRIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWQIGLANFVGIIDNHYPKTKIF
                     ENV OF AB047240      (4) LIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKTKIF
         TRANSLATION OF P386TOP-LINK      (1) ------------------------------------------------------------
          TRANSLATION OF POL349-LINK      (1) ---------------------------------------------------NHYPKTKIF
                LNCAP-GENOMEA-POLORF     (51) LIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKTKIF
TRANSLATION OF LNCAP-POL-GENA-GOODA     (51) LIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKTKIF
           TRANSLATION OF ORF111-10     (57) LIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKTKIF
                              PGD-P1     (17) ------------------------------------------------------------
                              PGD-P2      (1) ------------------------------------------------------------
                               PGDP3      (1) ------------------------------------------------------------
                           CONSENSUS    (301) LIGQ RLRII LCGNDPDKI VP  K QVRQAFI SGAW IGLANFLGIIDNHYPKTKIF
```

FIG. 8-3

```
                                          361                                                        420
            GI_4185939_EMB_CAA76879.1_  (358) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
            GI_4185943_EMB_CAA76882.1_  (361) QFLKMTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTQYQSAQRAELVAV
            GI_4185947_EMB_CAA76885.1_  (358) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
            GI_5931705_EMB_CAB56603.1_  (332) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKVAYTGPKERVIKTPYQSAQRAELVAV
                      ENV OF AB047240  (64) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
          TRANSLATION OF P386TOP-LINK   (1) ----------------------------GSSNGKAAYTGPKERVIKTPYQSAQRAELV--
           TRANSLATION OF POL349-LINK  (10) QFLKLTTWILPKITRREP------------------------------------------
                 LNCAP-GENOMEA-POLORF (111) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
TRANSLATION OF LNCAP-POL-GENA-GOODA (111) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
            TRANSLATION OF ORF111-10 (117) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
                               PGD-P1  (17) ------------------------------------------------------------
                               PGD-P2   (1) ---------------------------------KAAYTGPKERVIKTPC-----------
                                PGDP3   (1) ------------------------------------------------------------
                            CONSENSUS (361) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV

                                          421                                                        480
            GI_4185939_EMB_CAA76879.1_  (418) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYI
            GI_4185943_EMB_CAA76882.1_  (421) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYI
            GI_4185947_EMB_CAA76885.1_  (418) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYI
            GI_5931705_EMB_CAB56603.1_  (392) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYI
                      ENV OF AB047240 (124) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI
          TRANSLATION OF P386TOP-LINK  (31) ------------------------------------------------------------
           TRANSLATION OF POL349-LINK  (28) ------------------------------------------------------------
                 LNCAP-GENOMEA-POLORF (171) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI
TRANSLATION OF LNCAP-POL-GENA-GOODA (171) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI
            TRANSLATION OF ORF111-10 (177) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI
                               PGD-P1  (17) ------------------------------------------------------------
                               PGD-P2  (17) ------------------------------------------------------------
                                PGDP3   (1) ------------------------------------------------------------
                            CONSENSUS (421) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYS DD LNQLFNLLQQTVRKRNFPFYI
```

FIG. 8-4

```
                                              481                                                        540
           GI_4185939_EMB_CAA76879.1_  (478) THIRAHTNLPGPLTKANEQADLLVSSALIKAQELHALTHVNAAGLKNKFDVTWKQAKDIV
           GI_4185943_EMB_CAA76882.1_  (481) THIRAHTNLPGPLTKANEQADLLVSSALIKAQELHALTHVNVAGLKNKFDVTWKQAKDIV
           GI_4185947_EMB_CAA76885.1_  (478) THIRAHTNLPGPLTKANEQADLLVSSALIKAQELHALAHVNAAGLKNKFDVTWKQAKDIV
           GI_5931705_EMB_CAB56603.1_  (452) THIRAHTNLPGPLTKANEQADLLVSSAFIKAQELHALTHVNAAGLKNKFDVTWKQAKDIV
                      ENV OF AB047240  (184) THIRAHTNLPGPLTKANEQADLLVSSAFIKAQELLALTHVNAAGLKNKFDVTWKQAKDIV
          TRANSLATION OF P386TOP-LINK   (31) ------------------------------------------------------------
           TRANSLATION OF POL349-LINK   (28) ------------------------------------------------------------
                 LNCAP-GENOMEA-POLORF  (231) THIRAHTNLPGPLTKANEQADLLVSSAFIKAQELLALTHVNAAGLKNKFDVTWKQAKDIV
TRANSLATION OF LNCAP-POL-GENA-GOODA  (231) THIRAHTNLPGPLTKANEQADLLVSSAFIKAQELLALTHVNAAGLKNKFDVTWKQAKDIV
             TRANSLATION OF ORF111-10  (237) THIRAHTNLPGPLTKANEQADLLVSSAFIKAQELLALTHVNAAGLKNKFDVTWKQAKDIV
                               PGD-P1   (17) ------------------------------------------------------------
                               PGD-P2   (17) ------------------------------------------------------------
                                PGDP3    (1) ------------------------------------------------------------
                            CONSENSUS  (481) THIRAHTNLPGPLTKANEQADLLVSSA IKAQEL ALTHVNAAGLKNKFDVTWKQAKDIV

                                              541                                                        600
           GI_4185939_EMB_CAA76879.1_  (538) QHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWATC
           GI_4185943_EMB_CAA76882.1_  (541) QHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVSSFGRLSYIHVTVDTYSHFIWATC
           GI_4185947_EMB_CAA76885.1_  (538) QHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWATC
           GI_5931705_EMB_CAB56603.1_  (512) QHCTQCQVLDLPTQEAGVNPEVCVLMHYGKWMSHMYLHLGRLSYVHVTVDTYSHFMCATC
                      ENV OF AB047240  (244) QHCTQCQVLHLSTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC
          TRANSLATION OF P386TOP-LINK   (31) ------------------------------------------------------------
           TRANSLATION OF POL349-LINK   (28) ------------------------------------------------------------
                 LNCAP-GENOMEA-POLORF  (291) QHCTQCQVLHLSTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC
TRANSLATION OF LNCAP-POL-GENA-GOODA  (291) QHCTQCQVLHLSTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC
             TRANSLATION OF ORF111-10  (297) QHCTQCQVLHLSTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC
                               PGD-P1   (17) ------------------------------------------------------------
                               PGD-P2   (17) ------------------------------------------------------------
                                PGDP3    (1) ------------------------------------------------------------
                            CONSENSUS  (541) QHCTQCQVLHL TQEAGVNPRGLCPNALWQMD THV SFGRLSYVHVTVDTYSHFIWATC
```

FIG. 8-5

```
                                                601                                                        660
           GI_4185939_EMB_CAA76879.1_   (598) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
           GI_4185943_EMB_CAA76882.1_   (601) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
           GI_4185947_EMB_CAA76885.1_   (598) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
           GI_5931705_EMB_CAB56603.1_   (572) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
                      ENV OF AB047240   (304) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
          TRANSLATION OF P386TOP-LINK    (31) ------------------------------------------------------------
           TRANSLATION OF POL349-LINK    (28) ------------------------------------------------------------
                 LNCAP-GENOMEA-POLORF   (351) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
TRANSLATION OF LNCAP-POL-GENA-GOODA   (351) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
            TRANSLATION OF ORF111-10   (357) QTGESTSHAKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
                               PGD-P1    (17) ------------------------------------------------------------
                               PGD-P2    (17) ------------------------------------------------------------
                                PGDP3     (1) ------------------------------------------------------------
                            CONSENSUS   (601) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG

                                                661                                                        720
           GI_4185939_EMB_CAA76879.1_   (658) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT
           GI_4185943_EMB_CAA76882.1_   (661) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT
           GI_4185947_EMB_CAA76885.1_   (658) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT
           GI_5931705_EMB_CAB56603.1_   (632) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAE-HLT
                      ENV OF AB047240   (364) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAKQHLT
          TRANSLATION OF P386TOP-LINK    (31) ------------------------------------------------------------
           TRANSLATION OF POL349-LINK    (28) ------------------------------------------------------------
                 LNCAP-GENOMEA-POLORF   (411) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAKQHLT
TRANSLATION OF LNCAP-POL-GENA-GOODA   (411) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAKQHLT
            TRANSLATION OF ORF111-10   (417) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAKQHLT
                               PGD-P1    (17) ------------------------------------------------------------
                               PGD-P2    (17) ------------------------------------------------------------
                                PGDP3     (1) ---------------------------------------------------------HLT
                            CONSENSUS   (661) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSA QHLT
```

FIG. 8-6

```
                                             721                                                        780
         GI_4185939_EMB_CAA76879.1_   (718) GKKNSPHEGKLIWWKDSKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
         GI_4185943_EMB_CAA76882.1_   (721) GKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
         GI_4185947_EMB_CAA76885.1_   (718) GKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
         GI_5931705_EMB_CAB56603.1_   (691) GKKNSPHEGKLI------------------------------------------------
                    ENV OF AB047240   (424) GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
         TRANSLATION OF P386TOP-LINK   (31) ------------------------------------------------------------
          TRANSLATION OF POL349-LINK   (28) ------------------------------------------------------------
              LNCAP-GENOMEA-POLORF   (471) GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
TRANSLATION OF LNCAP-POL-GENA-GOODA   (471) GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
           TRANSLATION OF ORF111-10   (477) GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
                             PGD-P1    (17) ------------------------------------------------------------
                             PGD-P2    (17) ------------------------------------------------------------
                              PGDP3     (4) GKKNSPHEGKLIC-----------------------------------------------
                          CONSENSUS   (721) GKK SPHEGKLIWWKD KNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI

                                             781                                                        840
         GI_4185939_EMB_CAA76879.1_   (778) RDAKKSTSAETETS----------------------------------------------
         GI_4185943_EMB_CAA76882.1_   (781) GDAKKSTSAETETP----------------------------------------------
         GI_4185947_EMB_CAA76885.1_   (778) RDAKKSTSAETETS----------------------------------------------
         GI_5931705_EMB_CAB56603.1_   (703) ------------------------------------------------------------
                    ENV OF AB047240   (484) GDAKKRASTEMVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIVYRYP
         TRANSLATION OF P386TOP-LINK   (31) ------------------------------------------------------------
          TRANSLATION OF POL349-LINK   (28) ------------------------------------------------------------
              LNCAP-GENOMEA-POLORF   (531) GDAKKRASTEMVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIVYRYP
TRANSLATION OF LNCAP-POL-GENA-GOODA   (531) GDAKKRASTEMVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIVYRYP
           TRANSLATION OF ORF111-10   (537) GDAKKRASTEMVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIVYRYP
                             PGD-P1    (17) ------------------------------------------------------------
                             PGD-P2    (17) ------------------------------------------------------------
                              PGDP3    (17) ------------------------------------------------------------
                          CONSENSUS   (781)  DAKK  S E  T
```

FIG. 8-7

```
                                              841                                                        900
          GI_4185939_EMB_CAA76879.1_   (792) ------------------------------------------------------------
          GI_4185943_EMB_CAA76882.1_   (795) ------------------------------------------------------------
          GI_4185947_EMB_CAA76885.1_   (792) ------------------------------------------------------------
          GI_5931705_EMB_CAB56603.1_   (703) ------------------------------------------------------------
                     ENV OF AB047240   (544) PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNYLQDFSYQRSLKFR
          TRANSLATION OF P386TOP-LINK   (31) ------------------------------------------------------------
           TRANSLATION OF POL349-LINK   (28) ------------------------------------------------------------
                 LNCAP-GENOMEA-POLORF  (591) PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNYLQDFSYQRSLKFR
TRANSLATION OF LNCAP-POL-GENA-GOODA  (591) PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNYLQDFSYQRSLKFR
            TRANSLATION OF ORF111-10  (597) PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNYLQDFSYQRSLKFR
                               PGD-P1   (17) ------------------------------------------------------------
                               PGD-P2   (17) ------------------------------------------------------------
                                PGDP3   (17) ------------------------------------------------------------
                            CONSENSUS  (841)

                                              901                                                        960
          GI_4185939_EMB_CAA76879.1_   (792) ------------------------------------QSSTVDSQDEQNGDVRRTDEVAIH
          GI_4185943_EMB_CAA76882.1_   (795) ------------------------------------QSSTVDSQDEQNGDVRRTDEVAIH
          GI_4185947_EMB_CAA76885.1_   (792) ------------------------------------QSSTVDSQDEQNGDVRRTDEVAIH
          GI_5931705_EMB_CAB56603.1_   (703) ------------------------------------------------------------
                     ENV OF AB047240   (604) PKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQTQS
          TRANSLATION OF P386TOP-LINK   (31) ------------------------------------------------------------
           TRANSLATION OF POL349-LINK   (28) ------------------------------------------------------------
                 LNCAP-GENOMEA-POLORF  (651) PKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQTQS
TRANSLATION OF LNCAP-POL-GENA-GOODA  (651) PKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQTQS
            TRANSLATION OF ORF111-10  (657) PKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQTQS
                               PGD-P1   (17) ------------------------------------------------------------
                               PGD-P2   (17) ------------------------------------------------------------
                                PGDP3   (17) ------------------------------------------------------------
                            CONSENSUS  (901)                                        TI
```

FIG. 8-8

```
                                                   961                                                        1020
          GI_4185939_EMB_CAA76879.1_      (816)    QEGRAANLGTTKEADAVSYKISREHKGDTNPREYAACSLDDCINGGKSPYACRSSCS---
          GI_4185943_EMB_CAA76882.1_      (819)    QESRAADLGTTKEADAVSYKISREHKGDTNPREYAACGLDDCINGGKSPYACRSSCS---
          GI_4185947_EMB_CAA76885.1_      (816)    QEGRAANLGTTKEADAVSYKISREHKGDTNPREYAACSLDDCINGGKSPYACRSSCS---
          GI_5931705_EMB_CAB56603.1_      (703)    ------------------------------------------------------------
                     ENV OF AB047240      (664)    CPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPEIISPVSGPEHPELWR
        TRANSLATION OF P386TOP-LINK       (31)     ------------------------------------------------------------
         TRANSLATION OF POL349-LINK       (28)     ------------------------------------------------------------
               LNCAP-GENOMEA-POLORF       (711)    CPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPEIISPVSGP-------
TRANSLATION OF LNCAP-POL-GENA-GOODA       (711)    CPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPEIISPVSGPEHPELWR
          TRANSLATION OF ORF111-10        (717)    CPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPEIISPVSGPEHPELWR
                             PGD-P1       (17)     ------------------------------------------------------------
                             PGD-P2       (17)     ------------------------------------------------------------
                              PGDP3       (17)     ------------------------------------------------------------
                          CONSENSUS       (961)            A   D      K          P EWG   I        SP S

                                                   1021          1035
          GI_4185939_EMB_CAA76879.1_      (873)    ---------------
          GI_4185943_EMB_CAA76882.1_      (876)    ---------------
          GI_4185947_EMB_CAA76885.1_      (873)    ---------------
          GI_5931705_EMB_CAB56603.1_      (703)    ---------------
                     ENV OF AB047240      (724)    LWPDTTLEFGLEIKL
        TRANSLATION OF P386TOP-LINK       (31)     ---------------
         TRANSLATION OF POL349-LINK       (28)     ---------------
               LNCAP-GENOMEA-POLORF       (764)    ---------------
TRANSLATION OF LNCAP-POL-GENA-GOODA       (771)    LWPDTTLEFGLEIKL
          TRANSLATION OF ORF111-10        (777)    LWPDTTLEFGLEIKL
                             PGD-P1       (17)     ---------------
                             PGD-P2       (17)     ---------------
                              PGDP3       (17)     ---------------
                          CONSENSUS       (1021)
```

FIG. 8-9

```
                                   1                                                          60
    GI_4185940_EMB_CAA76880.1_  (1) ------------------------------------------------------------
    GI_4185944_EMB_CAA76883.1_  (1) ------------------------------------------------------------
    GI_4185948_EMB_CAA76886.1_  (1) ------------------------------------------------------------
    GI_5931706_EMB_CAB56604.1_  (1) ------------------------------------------------------------
               ENV OF AB047240  (1) MATLIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKT
  TRANSLATION OF E207TOP-LINK   (1) ------------------------------------------------------------
   TRANSLATION OF ENV287-LINK   (1) ------------------------------------------------------------
    TRANSLATION OF T20.22A-23   (1) ------------------------------------------------------------
                       PGD-E1   (1) ------------------------------------------------------------
                       PGD-E2   (1) ------------------------------------------------------------
                       PGD-E3   (1) ------------------------------------------------------------
                    CONSENSUS   (1)

                                   61                                                        120
    GI_4185940_EMB_CAA76880.1_  (1) ------------------------------------------------------------
    GI_4185944_EMB_CAA76883.1_  (1) ------------------------------------------------------------
    GI_4185948_EMB_CAA76886.1_  (1) ------------------------------------------------------------
    GI_5931706_EMB_CAB56604.1_  (1) ------------------------------------------------------------
               ENV OF AB047240 (61) KIFQFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAEL
  TRANSLATION OF E207TOP-LINK   (1) ------------------------------------------------------------
   TRANSLATION OF ENV287-LINK   (1) ------------------------------------------------------------
    TRANSLATION OF T20.22A-23   (1) ------------------------------------------------------------
                       PGD-E1   (1) ------------------------------------------------------------
                       PGD-E2   (1) ------------------------------------------------------------
                       PGD-E3   (1) ------------------------------------------------------------
                    CONSENSUS  (61)
```

FIG. 9-1

```
                                     121                                                        180
   GI_4185940_EMB_CAA76880.1_    (1) ------------------------------------------------------------
   GI_4185944_EMB_CAA76883.1_    (1) ------------------------------------------------------------
   GI_4185948_EMB_CAA76886.1_    (1) ------------------------------------------------------------
   GI_5931706_EMB_CAB56604.1_    (1) ------------------------------------------------------------
              ENV OF AB047240  (121) VAVITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFP
  TRANSLATION OF E207TOP-LINK    (1) ------------------------------------------------------------
   TRANSLATION OF ENV287-LINK    (1) ------------------------------------------------------------
    TRANSLATION OF T20.22A-23    (1) ------------------------------------------------------------
                       PGD-E1    (1) ------------------------------------------------------------
                       PGD-E2    (1) ------------------------------------------------------------
                       PGD-E3    (1) ------------------------------------------------------------
                    CONSENSUS  (121)

                                     181                                                        240
   GI_4185940_EMB_CAA76880.1_    (1) ------------------------------------------------------------
   GI_4185944_EMB_CAA76883.1_    (1) ------------------------------------------------------------
   GI_4185948_EMB_CAA76886.1_    (1) ------------------------------------------------------------
   GI_5931706_EMB_CAB56604.1_    (1) ------------------------------------------------------------
              ENV OF AB047240  (181) FYITHIRAHTNLPGPLTKANEQADLLVSSAFIKAQELLALTHVNAAGLKNKFDVTWKQAK
  TRANSLATION OF E207TOP-LINK    (1) ------------------------------------------------------------
   TRANSLATION OF ENV287-LINK    (1) ------------------------------------------------------------
    TRANSLATION OF T20.22A-23    (1) ------------------------------------------------------------
                       PGD-E1    (1) ------------------------------------------------------------
                       PGD-E2    (1) ------------------------------------------------------------
                       PGD-E3    (1) ------------------------------------------------------------
                    CONSENSUS  (181)
```

FIG. 9-2

```
                                  241                                                        300
 GI_4185940_EMB_CAA76880.1_    (1) ------------------------------------------------------------
 GI_4185944_EMB_CAA76883.1_    (1) ------------------------------------------------------------
 GI_4185948_EMB_CAA76886.1_    (1) ------------------------------------------------------------
 GI_5931706_EMB_CAB56604.1_    (1) ------------------------------------------------------------
            ENV OF AB047240  (241) DIVQHCTQCQVLHLSTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIW
TRANSLATION OF E207TOP-LINK    (1) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK    (1) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23    (1) ------------------------------------------------------------
                     PGD-E1    (1) ------------------------------------------------------------
                     PGD-E2    (1) ------------------------------------------------------------
                     PGD-E3    (1) ------------------------------------------------------------
                  CONSENSUS  (241)

                                  301                                                        360
 GI_4185940_EMB_CAA76880.1_    (1) ------------------------------------------------------------
 GI_4185944_EMB_CAA76883.1_    (1) ------------------------------------------------------------
 GI_4185948_EMB_CAA76886.1_    (1) ------------------------------------------------------------
 GI_5931706_EMB_CAB56604.1_    (1) ------------------------------------------------------------
            ENV OF AB047240  (301) ATCQTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYN
TRANSLATION OF E207TOP-LINK    (1) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK    (1) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23    (1) ------------------------------------------------------------
                     PGD-E1    (1) ------------------------------------------------------------
                     PGD-E2    (1) ------------------------------------------------------------
                     PGD-E3    (1) ------------------------------------------------------------
                  CONSENSUS  (301)
```

FIG. 9-3

```
                                       361                                                       420
  GI_4185940_EMB_CAA76880.1_     (1) --------------------------MQRKAPPRRRRHRNRAPLTHKMNKMVTSEEQMKL
  GI_4185944_EMB_CAA76883.1_     (1) --------------------------MQRKAPPRRRRHRNRAPLTHKMNKMVTSEEQMKL
  GI_4185948_EMB_CAA76886.1_     (1) --------------------------MQRKAPPRRRRHRNRAPLTHKMNKMVTSEEQMKL
  GI_5931706_EMB_CAB56604.1_     (1) ------------------------------------------------------------
             ENV OF AB047240   (361) SQGQAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAKQ
 TRANSLATION OF E207TOP-LINK     (1) ------------------------------------------------------------
  TRANSLATION OF ENV287-LINK     (1) ------------------------------------------------------------
   TRANSLATION OF T20.22A-23     (1) ---------------------MNPSEMQRKAPPRRRRHRNRAPLTHKMNKMVTSEEQMKL
                      PGD-E1     (1) ------------------------------------------------------------
                      PGD-E2     (1) ------------------------------------------------------------
                      PGD-E3     (1) ------------------------------------------------------------
                   CONSENSUS   (361)

                                       421                                                       480
  GI_4185940_EMB_CAA76880.1_    (35) PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVSLPMPAGAAAA
  GI_4185944_EMB_CAA76883.1_    (35) PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVSLPMPAGAAAA
  GI_4185948_EMB_CAA76886.1_    (35) PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVSLPMPAGAAAA
  GI_5931706_EMB_CAB56604.1_     (1) ------------------------------------------------------------
             ENV OF AB047240   (421) HLTGKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYN
 TRANSLATION OF E207TOP-LINK     (1) ------------------------------------------------------------
  TRANSLATION OF ENV287-LINK     (1) ------------------------------------------------------------
   TRANSLATION OF T20.22A-23    (40) PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVSLPMPAGAAAA
                      PGD-E1     (1) ------------------------------------------------------------
                      PGD-E2     (1) ------------------------------------------------------------
                      PGD-E3     (1) ------------------------------------------------------------
                   CONSENSUS   (421)
```

FIG. 9-4

```
                                     481                                                        540
     GI_4185940_EMB_CAA76880.1_   (95) NYTYWAYVPFPP-LIRAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGY
     GI_4185944_EMB_CAA76883.1_   (95) NYTYWAYVPFPP-LIRAVTWMDNPIEVYVNDSVWVPGPTDDHCPAKPEEEGMMINISIGY
     GI_4185948_EMB_CAA76886.1_   (95) NYTYWAYVPFPP-LIRAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGY
     GI_5931706_EMB_CAB56604.1_    (1) -------------MVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIGY
                ENV OF AB047240  (481) EPIGDAKKRASTEMVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIVY
   TRANSLATION OF E207TOP-LINK     (1) ------------------------------------------------------------
    TRANSLATION OF ENV287-LINK     (1) ------------------------------------------------------------
     TRANSLATION OF T20.22A-23   (100) NYTYWAYVPFPP-LIRAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGY
                        PGD-E1     (1) ------------------------------------------------------------
                        PGD-E2     (1) ------------------------------------------------------------
                        PGD-E3     (1) ------------------------------------------------------------
                     CONSENSUS   (481)              LI  VTWMDNP EVYVNDSVWVPGP DD CPAKPEEEGMMINISI Y

                                     541                                                        600
     GI_4185940_EMB_CAA76880.1_  (154) HYPPICLGRAPGCLMPAVQNWLVEVPTVSPICRFTYHMVSGMSLRPRVNYLQDFSYQRSL
     GI_4185944_EMB_CAA76883.1_  (154) RYPPICLGRAPGCLMPAVQNWLVEVPTVSPISRFTYHMVSGMSLRPRVNYLQDFSYQRSF
     GI_4185948_EMB_CAA76886.1_  (154) HYPPICLGRAPGCIMPAVQNWLVEVPTVSPICRFTYHMVSGMSLRPRVNYLQDFSYQRSL
     GI_5931706_EMB_CAB56604.1_   (48) HYPPICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNCLQDFSYQRSL
                ENV OF AB047240  (541) RYPPICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNYLQDFSYQRSL
   TRANSLATION OF E207TOP-LINK     (1) -----------------------------------------------------FSYQRSL
    TRANSLATION OF ENV287-LINK     (1) ------------------------------------------------------------
     TRANSLATION OF T20.22A-23   (159) HYPPICLGRAPGCLMPAVQNWLVEVPTVSPICRFTYHMVSGMSLRPRVNYLQDFSYQRSL
                        PGD-E1     (1) ------------------------------------------------------------
                        PGD-E2     (1) ------------------------------------------------------------
                        PGD-E3     (1) ------------------------------------------------------------
                     CONSENSUS   (541)  YPPICLGRAPGCLMPAVQNWLVEVPTVSP  RFTYHMVSGMSLRPRVN LQDFSYQRSL
```

FIG. 9-5

```
                                    601                                                        660
  GI_4185940_EMB_CAA76880.1_  (214) KFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQ
  GI_4185944_EMB_CAA76883.1_  (214) KFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQ
  GI_4185948_EMB_CAA76886.1_  (214) KFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQ
  GI_5931706_EMB_CAB56604.1_  (108) KFRPKGKTCPKEIPKGSKNTEVLVWEECVANSVVILQNNEFGTIIDWAPRGQFYHNCSGQ
             ENV OF AB047240  (601) KFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQ
 TRANSLATION OF E207TOP-LINK    (8) KFRPKGKPCPKEIPKESKNTEVL-------------------------------------
  TRANSLATION OF ENV287-LINK    (1) ------------------------------------------------------------
   TRANSLATION OF T20.22A-23  (219) KFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQ
                      PGD-E1    (1) --RPKGKPCPKEIPKESC------------------------------------------
                      PGD-E2    (1) ------------------------------------------------------------
                      PGD-E3    (1) ------------------------------------------------------------
                   CONSENSUS  (601) KFRPKGKPCPKEIPKESKNTEVLVWEECVANS VILQNNEFGTIIDWAPRGQFYHNCSGQ

                                    661                                                        720
  GI_4185940_EMB_CAA76880.1_  (274) TQSCQSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPKIVSPVSGPEHPE
  GI_4185944_EMB_CAA76883.1_  (274) TQSCPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPKIISPVSGPEHPE
  GI_4185948_EMB_CAA76886.1_  (274) TQSCPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPKIVSPVSGPEHPE
  GI_5931706_EMB_CAB56604.1_  (168) TQSCPSAQVSPAVDSDLTESLDKHKHKKLQSFYLWEWEEKGISTPRPKIISPVSGPEHPE
             ENV OF AB047240  (661) TQSCPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPEIISPVSGPEHPE
 TRANSLATION OF E207TOP-LINK   (31) ------------------------------------------------------------
  TRANSLATION OF ENV287-LINK    (1) --------------SDLTESLDKHKHKKLQSFYPWEWGEKGI------------------
   TRANSLATION OF T20.22A-23  (279) TQSCPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPKIVSPVSGPEHPE
                      PGD-E1   (17) ------------------------------------------------------------
                      PGD-E2    (1) ------------------------------------------------------------
                      PGD-E3    (1) ------------------------------------------------------------
                   CONSENSUS  (661) TQSC SAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRP IISPVSGPEHPE
```

FIG. 9-6

```
                                     721                                                        780
   GI_4185940_EMB_CAA76880.1_ (334) LWRLTVASHHIRIWSGNQTLETRDRKPFYTIDLNSSLTVPLQSCVKPPYMLVVGNIVIKP
   GI_4185944_EMB_CAA76883.1_ (334) LWRLTVASHHIRIWSGNQTLETRDRKPFYTVDLNSSVTVPLQSCIKPPYMLVVGNIVIKP
   GI_4185948_EMB_CAA76886.1_ (334) LWRLTVASHHIRIWSGNQTLETRDRKPFYTIDLNSSLTVPLQSCVKPPYMLVVGNIVIKP
   GI_5931706_EMB_CAB56604.1_ (228) LWRLTVASHHIRIWSGNQTLETRYRKPFYTIDLNSILTVPLQSCVKPPYMLVVGNIVIKP
              ENV OF AB047240 (721) LW---------RL---------------------W---------------------P---
 TRANSLATION OF E207TOP-LINK   (31) ------------------------------------------------------------
  TRANSLATION OF ENV287-LINK   (29) ------------------------------------------------------------
   TRANSLATION OF T20.22A-23  (339) LWRLTVASHHIRIWSGNQTLETRDRKPFYTIDLNSSLTVPLQSCVKPPYMLVVGNIVIKP
                      PGD-E1   (17) ------------------------------------------------------------
                      PGD-E2    (1) --------------------------------LNSSLTVPLQSCVKPC------------
                      PGD-E3    (1) ------------------------------------------------------------
                   CONSENSUS  (721) LW         RI                    LNS LTVPLQSCVKP

                                     781                                                        840
   GI_4185940_EMB_CAA76880.1_ (394) DSQTITCENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWEASPSVHILTEVLKG
   GI_4185944_EMB_CAA76883.1_ (394) DSQTITCENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWETSPSIHTLTEVLKG
   GI_4185948_EMB_CAA76886.1_ (394) DSQTITCENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWEASPSVHILTEVLKG
   GI_5931706_EMB_CAB56604.1_ (288) ASQTITCENCRLFTCIDSTFNWQHRILLVRAREGMWIPVSTDRPWEASPSIHILTEILKG
              ENV OF AB047240 (727) ----------------DTTLEFGLEIKL--------------------------------
 TRANSLATION OF E207TOP-LINK   (31) ------------------------------------------------------------
  TRANSLATION OF ENV287-LINK   (29) ------------------------------------------------------------
   TRANSLATION OF T20.22A-23  (399) DSQTITCENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWEASPSVHILTEVLKG
                      PGD-E1   (17) ------------------------------------------------------------
                      PGD-E2   (17) ------------------------------------------------------------
                      PGD-E3    (1) ------------------------------------------------------------
                   CONSENSUS  (781)                 DST  W   I L
```

FIG. 9-7

```
                                     841                                                        900
GI_4185940_EMB_CAA76880.1_    (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI
GI_4185944_EMB_CAA76883.1_    (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI
GI_4185948_EMB_CAA76886.1_    (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI
GI_5931706_EMB_CAB56604.1_    (348) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNYWQKNSTRLWNSQSSI
           ENV OF AB047240    (739) ------------------------------------------------------------
TRANSLATION OF E207TOP-LINK    (31) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK    (29) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23   (459) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI
                     PGD-E1    (17) ------------------------------------------------------------
                     PGD-E2    (17) ------------------------------------------------------------
                     PGD-E3     (1) ------------------------------------------------------------
                  CONSENSUS   (841)

                                     901                                                        960
GI_4185940_EMB_CAA76880.1_    (514) DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH
GI_4185944_EMB_CAA76883.1_    (514) DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFSITPQIYNESEHHWDMVRRH
GI_4185948_EMB_CAA76886.1_    (514) DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESELHWDMVRRH
GI_5931706_EMB_CAB56604.1_    (408) DQKLASQINDLRQTVIWMGDRLMTLEHHFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH
           ENV OF AB047240    (739) ------------------------------------------------------------
TRANSLATION OF E207TOP-LINK    (31) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK    (29) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23   (519) DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH
                     PGD-E1    (17) ------------------------------------------------------------
                     PGD-E2    (17) ------------------------------------------------------------
                     PGD-E3     (1) ------------------------------------------------------------
                  CONSENSUS   (901)
```

FIG. 9-8

```
                                    961                                                        1020
GI_4185940_EMB_CAA76880.1_   (574) LQGREDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTTI
GI_4185944_EMB_CAA76883.1_   (574) LQGREDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTTI
GI_4185948_EMB_CAA76886.1_   (574) LQGREDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTTI
GI_5931706_EMB_CAB56604.1_   (468) LQGREDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWIKTIRSTMI
           ENV OF AB047240   (739) ------------------------------------------------------------
TRANSLATION OF E207TOP-LINK   (31) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK   (29) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23  (579) LQGREDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTTI
                     PGD-E1   (17) ------------------------------------------------------------
                     PGD-E2   (17) ------------------------------------------------------------
                     PGD-E3    (1) ------------------------------------------------------------
                  CONSENSUS  (961)

                                    1021                                                        1081
GI_4185940_EMB_CAA76880.1_   (634) INLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV
GI_4185944_EMB_CAA76883.1_   (634) INLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV
GI_4185948_EMB_CAA76886.1_   (634) INLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV
GI_5931706_EMB_CAB56604.1_   (528) INLILIVVCLFCLLLVCRCTQQLRRDSDIENGP----------------------------
           ENV OF AB047240   (739) -------------------------------------------------------------
TRANSLATION OF E207TOP-LINK   (31) -------------------------------------------------------------
 TRANSLATION OF ENV287-LINK   (29) -------------------------------------------------------------
  TRANSLATION OF T20.22A-23  (639) INLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV
                     PGD-E1   (17) -------------------------------------------------------------
                     PGD-E2   (17) -------------------------------------------------------------
                     PGD-E3    (1) -----------------RCTQQLRRDSDHRERA----------------------------
                  CONSENSUS (1021)                  RCTQQLRRDSD
```

FIG. 9-9